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92661

From: Huff, Sheela  
Sent: Monday, April 28, 2003 4:44 PM  
To: STIC-Biotech/ChemLib  
Subject: search request for 09/682667

Please search and interference search SEQ ID No. 2, 4, 6, and 8 of the above application.

Thanks-

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CMI-8307  
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CRIE

Point of Contact  
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Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 5/1/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:19:46 ; Search time 27.2507 Seconds  
(without alignments)  
1610.532 Million cell updates/sec

Title: US-09-682-667-2

Perfect score: 1094

Sequence: 1 MEVLRRSSVFPAEIMDAFDR.....TLCSPGRFLKAFELLPER 213

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organeller:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioplasmid:\*  
17: sp\_archaeoplasmid:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1094	100.0	213	11 035425	035425 ratu
2	1076	98.4	213	4 09UR32	09UR32 homo sapien
3	1035.5	94.7	212	4 09URX3	09URX3 homo sapien
4	892	81.5	213	13 091812	091812 gallus galli
5	886	81.0	213	13 09DGJ5	09DGJ5 gallus galli
6	846.5	77.4	170	11 088857	088857 rattus norv
7	244.5	22.3	300	5 09V9C8	09V9C8 drosophila
8	243.5	22.3	309	5 08TR85	08TR85 drosophila
9	243.5	22.3	313	5 09NEX3	09NEX3 drosophila
10	234	19.4	247	5 09V612	09V612 drosophila
11	213.5	19.5	317	5 095083	095083 drosophila
12	159	14.5	235	11 035843	035843 mus musculu
13	155	14.2	236	11 0923R6	0923R6 cricetus
14	154.5	14.1	188	11 09QWXX2	09QWXX2 mus musculu
15	154.5	14.1	233	11 035844	035844 mus musculu
16	151.5	13.8	233	6 09MGS7	09MGS7 ovis aries

17	151.5	13.8	233	6 09N1A2	09N1A2 sus scrofa
18	150.5	13.8	188	4 09H1R6	09H1R6 homo sapien
19	150.5	13.8	233	6 08S042	08S042 felis silve
20	148.5	13.6	192	13 0919N4	0919N4 brachydanio
21	147.5	13.5	219	11 09N936	09N936 mus musculu
22	146.5	13.4	179	4 09N937	09N937 homo sapien
23	146.5	13.4	233	6 09N936	09N936 mus musculu
24	146.5	13.3	238	13 090298	090298 brachydanio
25	143	13.1	217	11 090298	090298 mus musculu
26	139.5	12.8	204	13 0902H2	0902H2 xenopus lae
27	138.5	12.7	163	6 09M2S6	09M2S6 ovis aries
28	138.5	12.7	173	4 08W249	08W249 homo sapien
29	138.5	12.7	180	6 09BD05	09BD05 bos taurus
30	137	12.5	221	13 09N013	09N013 xenopus lae
31	136.5	12.5	180	6 09N013	09N013 bos taurus
32	135.5	12.4	193	11 088996	088996 rattus norv
33	134	12.2	192	6 08S043	08S043 felis silve
34	134	12.2	209	11 09JY59	09JY59 rattus norv
35	133.5	12.2	178	11 09CYW5	09CYW5 mus musculu
36	132.5	12.1	149	6 09G0G7	09G0G7 ovis aries
37	127.5	11.7	330	11 0921P3	0921P3 rattus norv
38	127	11.6	331	11 097287	097287 mus musculu
39	125	11.4	173	11 09UKL3	09UKL3 rattus norv
40	117	10.7	211	13 09W6F1	09W6F1 gallus galli
41	117	10.7	350	4 09UNJ1	09UNJ1 homo sapien
42	111.5	10.2	114	4 09NR76	09NR76 homo sapien
43	102.5	9.4	172	11 055177	055177 mus musculu
44	99	9.0	172	11 055179	055179 mus musculu
45	98.5	9.0	89	13 08W0J1	08W0J1 gallus galli

## ALIGNMENTS

## RESULT 1

035425 ID 035425 PRELIMINARY; PRT; 213 AA.  
AC 035425;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE BCL-2-related ovarian killer protein.  
GN BOK OR BOKL OR BOK OR MTD.  
OS Rattus norvegicus (Rat), and  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116, 10050;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat: STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;  
RX MEDLINE=98024143; Pubmed=9356461;  
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
RT "Box is a pro-apoptotic Bcl-2 protein with restricted expression in  
RT reproductive tissues and heterodimerizes with selective anti-apoptotic  
RT Bcl-2 family members."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat: STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;  
RA Hsu S.Y., Hsueh A.J.W.;  
RX Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Mouse;  
RA Inohara N., Ekhterae D., Garcia I., Carrio R., Merino J., Merry A.,  
RA Chen S., Nunez G.;  
RX Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF027954; AAB87418.1; -  
DR EMBL: AF027707; AAC3582.1; -  
DR MGD: MGI:1858494; BOK.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; BCL2\_family.

DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL2\_FAMILY; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

Query Match 100.0%; Score 1094; DB 11; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-88;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRLRAGLSWSPERASAP 60
DB 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRLRAGLSWSPERASAP 60
OY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHLPLOSEPVYTDFAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHLPLOSEPVYTDFAFLAVAGHIFSAGIT 120
OY 121 WGVVSLYSVAAGLAVDCVROQAPAMVHALVDCLEFVYKTLATWLRRGWTDVLCYV 180
DB 121 WGVVSLYSVAAGLAVDCVROQAPAMVHALVDCLEFVYKTLATWLRRGWTDVLCYV 180
OY 181 STDGFRSHMLVATLCSFGFRLKAAFFLLPPER 213
DB 181 STDGFRSHMLVATLCSFGFRLKAAFFLLPPER 213

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## RESULT 2

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OY 09UL32 PRELIMINARY; PRT; 213 AA.
AC 09UL32:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-2 related ovarian killer.
GN BOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsu S.Y., Hsueh A.J.W.;
RT "CDNA cloning of the human BOK gene";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF089746; AAF09129.1; -.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL2_FAMILY; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 213 AA; 23540 MW; 59509F8C7330517F CRC64;

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Query Match 98.4%; Score 1076; DB 4; Length 213;  
 Best Local Similarity 98.6%; Pred. No. 7.2e-87;  
 Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRLRAGLSWSPERASAP 60
DB 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRLRAGLSWSPERASAP 60
OY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHLPLOSEPVYTDFAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHLPLOSEPVYTDFAFLAVAGHIFSAGIT 120
OY 121 WGVVSLYSVAAGLAVDCVROQAPAMVHALVDCLEFVYKTLATWLRRGWTDVLCYV 180
DB 121 WGVVSLYSVAAGLAVDCVROQAPAMVHALVDCLEFVYKTLATWLRRGWTDVLCYV 180
OY 181 STDGFRSHMLVATLCSFGFRLKAAFFLLPPER 213
DB 181 STDGFRSHMLVATLCSFGFRLKAAFFLLPPER 213

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## RESULT 3

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OY 09UMX3 PRELIMINARY; PRT; 212 AA.
AC 09UMX3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BCL-2-related ovarian killer protein (Similar to BCL-2-related ovarian
DE killer protein-like-PENDING) (BCL-2-related ovarian killer
DE protein-like).
GN BOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H.;
RT "Gene expression of a human homolog of BCL-2-related ovarian killer
RT protein.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174487; AAD51719.1; -.
DR EMBL; BC006203; AAH06203.1; -.
DR EMBL; BC017214; AAH17214.1; -.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL2_FAMILY; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 212 AA; 23280 MW; 053ED605FE8F5B2 CRC64;

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Query Match 94.7%; Score 1035.5; DB 4; Length 212;  
 Best Local Similarity 95.3%; Pred. No. 2.6e-83;  
 Matches 203; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

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OY 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRLRAGLSWSPERASAP 60
DB 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRLRAGLSWSPERASAP 60
OY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHLPLOSEPVYTDFAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHLPLOSEPVYTDFAFLAVAGHIFSAGIT 119
OY 121 WGVVSLYSVAAGLAVDCVROQAPAMVHALVDCLEFVYKTLATWLRRGWTDVLCYV 180
DB 121 WGVVSLYSVAAGLAVDCVROQAPAMVHALVDCLEFVYKTLATWLRRGWTDVLCYV 179
OY 181 STDGFRSHMLVATLCSFGFRLKAAFFLLPPER 213
DB 181 STDGFRSHMLVATLCSFGFRLKAAFFLLPPER 212

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## RESULT 4

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OY 091812 PRELIMINARY; PRT; 213 AA.
AC 091812:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-2-related ovarian killer protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

```



OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487164; PubMed=11034351.  
 RA Zhang H., Holzgrevé W., De Geyter C.;  
 RT "Evolutionarily conserved Bcl proteins in the Bcl-2 family."  
 RL FEBS Lett. 480:311-313(2000).  
 DR EMBL; AF275944; AAF81282.1;  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; P550062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23619 MW; B3AF7049P25442E3 CRC64;

Query Match 81.5%; Score 892; DB 13; Length 213;  
 Best Local Similarity 78.4%; Pred. No. 1,le-70;  
 Matches 167; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASPP 60  
 DB 1 MEVLRRSSVFAAEVMEVFRSPTDKELVQAQALCRDYINSRLIRAGVSMSPKPHNTPPV 60  
 OY 61 GGRLAEVCVTLRLDGELEQIRPSYRNAROLHPILOSEPVYTDALFLAVAGHISAGIT 120  
 DB 61 GGRLAEVSAILLRLDGELEYIRPNRYRNAROLNLSHSETVYTDALFLAVAAQIFTAGIT 120  
 OY 121 WGVVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
 DB 121 WGVVSVLSVAAGLAVDCVROQAPAMVHITVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
 OY 181 STDGFRSHMLVATLCSFGFRLKAAFFLLP 213  
 DB 181 STDPSLRSHMLVAAVCSFGHFLKAFVLLP 213

RESULT 5  
 OY 09DGCJ5 PRELIMINARY; PRT; 213 AA.  
 ID 09DGCJ5;  
 AC 09DGCJ5;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Bcl-2-related ovarian killer protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Mills E.M., Johnson A.L., Bridgham J.T.;  
 RT "Characterization and Expression of Bok in the Hen Ovary."  
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF290888; AAG0182.1;  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_FAMILY.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; P550062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23658 MW; 07CC06BEBD7311EC CRC64;

Query Match 81.0%; Score 886; DB 13; Length 213;  
 Best Local Similarity 77.5%; Pred. No. 3,6e-70;  
 Matches 165; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASPP 60  
 DB 1 MEVLRRSSVFAAEVMEVFRSPTDKELVQAQALCRDYINSRLIRAGVSMSPKPHNTPPV 60  
 OY 61 GGRLAEVCVTLRLDGELEQIRPSYRNAROLHPILOSEPVYTDALFLAVAGHISAGIT 120  
 DB 61 GGRLAEVSAILLRLDGELEYIRPNRYRNAROLNLSHSETVYTDALFLAVAAQIFTAGIT 120

DB 61 GGRLAEVSAILLRLDGELEYIRPNRYRNAROLNLSHSETVYTDALFLAVAAQIFTAGIT 120  
 OY 121 WGVVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
 DB 121 WGVVSVLSVAAGLAVDCVROQAPAMVHITVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
 OY 181 STDGFRSHMLVATLCSFGFRLKAAFFLLP 213  
 DB 181 STDPSLRSHMLVAAVCSFGHFLKAFVLLP 213

RESULT 6  
 ID 088857 PRELIMINARY; PRT; 170 AA.  
 AC 088857;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Bcl-2-related ovarian killer protein.  
 GN BOK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=OVARY;  
 RC TISSUE=OVARY;  
 RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
 RT "Bok is a pro-apoptotic bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic bcl-2 family members."  
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=OVARY;  
 RA Hsu S.Y., Hsueh A.J.W.;  
 RT "A splicing variant of the Bcl-2 member Bok with a truncated BH3 domain induces apoptosis without dimerization with anti-apoptotic Bcl-2 proteins."  
 RT Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF051093; AAC61928.1;  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_FAMILY.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; P550062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

Query Match 77.4%; Score 846.5; DB 11; Length 170;  
 Best Local Similarity 79.8%; Pred. No. 8,2e-67;  
 Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASPP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASPP 60  
 OY 61 GGRLAEVCVTLRLDGELEQIRPSYRNAROLHPILOSEPVYTDALFLAVAGHISAGIT 120  
 DB 61 GGRLAEVCVTLRLDGELEQIRPSYRNAROLHPILOSEPVYTDALFLAVAGHISAGIT 120  
 OY 121 WGVVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
 DB 121 WGVVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
 OY 181 STDGFRSHMLVATLCSFGFRLKAAFFLLP 213  
 DB 181 STDGFRSHMLVATLCSFGFRLKAAFFLLP 213

RESULT 7  
 ID 09Y9C8 PRELIMINARY; PRT; 300 AA.  
 ID 09Y9C8

AC Q9V9C8; 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE DEBCL1 (BCL-2 family member protein) (BCL-2 ORFHOLOG: DBORG-1).  
 GN DEBCL1 OR DBORG1 OR BOK OR BCL2 OR BGL OR ROB-1 OR CG12397.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid:7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-EMBRYO;  
 RX MEDLINE-20105529; PubMed-2015529;  
 RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Nunez G., Okano H.,  
 RA Miura M.;  
 RT "Drob-1, a Drosophila member of the Bcl-2/CED-9 family that promotes  
 RT cell death.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:662-667(2000).  
 RN [2]  
 RP REVISIONS TO N-TERMINUS.  
 RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Okano H., Miura M.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20155310; PubMed-10684252;  
 RA Couseli P.A., Quinn L.M., Huang D.C.S., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RT "Debel, a proapoptotic Bcl-2 homologue, is a component of the  
 RT Drosophila melanogaster cell death machinery.";  
 RL J. Cell Biol. 148:703-714(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Zhang H., Huang Q., Ke N., Matsuyama S., Hammock B., Godzik A.,  
 RA Reed J.C.;  
 RT "Drosophila pro-apoptotic Bcl-2/Bax homologue reveals evolutionary  
 RT conservation of cell death mechanisms.";  
 RL J. Biol. Chem. 0:0-0(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherier S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolishkov S.,  
 RA Botkay D., Botchan M.R., Boulton J., Brokstein P., Brotlier P.,  
 RA Butts K.C., Busam D.A., Butler H., Cardew E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Paulos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Doonan K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idagyan C.,  
 RA Jaitai B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Palzer K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodedge T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.-N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Kurada P., White K.;  
 RT "Putative Drosophila homolog of mammalian Bcl-2-related ovarian killer  
 RT protein.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Zhou L., Steller H.;  
 RT "Potential Drosophila homologue of Bcl-2-related ovarian killer  
 RT (BOK).";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Brachmann C.B., Jaasim O.W., Wachsmuth B.D., Cagan R.L.;  
 RT "Drob-1, a Drosophila Bcl-2 family member that functions in the  
 RT apoptotic response to UV-irradiation.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB032430; BAA89603.2; -;  
 DR EMBL; AF149798; AAF26841.1; ALT\_INIT.  
 DR EMBL; AF178430; AAF26289.1; -;  
 DR EMBL; AF228044; AAF89165.1; -;  
 DR EMBL; AE003789; AAF57365.1; ALT\_TERM.  
 DR EMBL; AF216752; AAF25955.1; ALT\_TERM.  
 DR EMBL; AF244352; AAF44324.1; -;  
 DR EMBL; AF244352; AAF44714.1; -;  
 DR FLYbase; FBgn0029131; debcl.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR000822; Znf\_C2H2.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PSS0157; ZINC\_FINGER\_C2H2\_2; 4.  
 DR DNA-binding; zinc-finger.  
 KW CONFLICT 1 86 MISSING (IN REF. 4).  
 FT FT 215 215 I -> V (IN REF. 1).  
 FT FT 217 217 C -> R (IN REF. 4).  
 SO SEQUENCE 300 AA; 32940 MW; FE29B0ADCF3D0942 CRC64;  
 Query Match 22.3%; Score 244.5; DB 5; Length 300;  
 Best local similarity 35.9%; Pred. No. 1.4e-13;  
 Matches 56; Conservative 27; Mismatches 64; Indels 9; Gaps 4;  
 QY 26 ELVQAQKALGREYVARLLRAG-LSWSAPER-----ASPAQGRILAECTVLRGDELEQ 80  
 DB 96 DIINGKCLGCGYIRARRRAGVLRNKTQRLNIDLDGSSHYVEVPALNSGDELER 155  
 QY 81 IRPSYRNVAQOL-HIP---LQSEPVYDAFLAVAGHIFSGITGWKYSLSYVAAGLAV 136  
 DB 156 MHPRYTINISQLSRAPGELEDSMDAMMLNLVAKDLFRSSITWGIISIFAVCGGPAI 215  
 QY 137 DCVRQAPAMHALVDCGFEVFKTLATWLRRGW 172  
 DB 216 DCVRGHEFDYDGLDGLAEITEDLVYWLIDNGW 251  
 RESULT 8  
 ID 0878Y5 PRELIMINARY; PRT: 299 AA.  
 AC 0878Y5;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE AT16536p.  
GN BUFFY.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,  
RA Chame M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guatin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Munhall C.J., Nuncio J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celinker S.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: A075219; AAL68086.1; -  
SQ SEQUENCE 299 AA; 33379 MW; 7FB125A6B7323B23 CRC64;

Query Match 22.3%; Score 243.5; DB 5; Length 299;  
Best Local Similarity 31.1%; Pred. No. 1.7e-13;  
Matches 66; Conservative 35; Mismatches 80; Indels 31; Gaps 8;

OY 25 KEIQAQKALGREGYVARLIRACL--SWSAPERASAPG---GRLAEVCTVLLRGDEL 78  
DB 87 ODIISQRCICGHIKIRRLRSGLFNKIKLQIRISILGSGTSGIYADVPAQVGLDEL 146  
OY 79 EOIRPSVYRNVARQL-----HIPLOSEPVTDAFLAVAGHIFSGATMGVSLYSV 130  
DB 147 ERNHPRIYNGVARQICRNPGGEHTP---DAVSLILGAGRELFRVEITWSVLSIFAI 202  
OY 131 AAGLAVCYROAPAMVHALVDCIGFVRKTLATWLRRCGW---TDVLKCVSTDPGF 186  
DB 203 AGSLSDVCYRQGHPEYLPKLMESVYEIDELVPMINENCGSGINTHVLPNTSLNP-- 260  
OY 187 RSHWLVAITL-CSRG-----RFLKAFFLLPE 212  
DB 261 -LEMTLVIGVGFGLLVEMILFRIFNLIVPK 291

## RESULT 9

ID 09NGX3 PRELIMINARY; PRT; 313 AA.  
AC 09NGX3;  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Bcl-2-like protein BUFFY (Fragment).  
GN BUFFY OR CG8238.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-20153510; PubMed-10684252;  
RA Colussi P.A., Quinn L.M., Huang D.C., Coombe M., Read S.H.,  
RA Richardson H., Kumar S.;  
RL "Drosophila melanogaster cell death machinery.",  
RT Drosophila melanogaster cell death machinery.",  
RL J. Cell Biol. 148:703-714(2000).  
DR EMBL: AF237864; AAF44120.1; -  
DR HSSP: 007817; IMA2.  
DR FLYbase: FBgn0040491; BUFFY.  
DR InterPro: IPR000712; BCL2-BH.  
DR InterPro: IPR002475; BCL2\_Family.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL; 1.  
DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 313 AA; 34909 MW; 775A41FDD05B678E CRC64;

Query Match 22.3%; Score 243.5; DB 5; Length 313;  
Best Local Similarity 31.1%; Pred. No. 1.7e-13;  
Matches 66; Conservative 35; Mismatches 80; Indels 31; Gaps 8;

OY 25 KEIQAQKALGREGYVARLIRACL--SWSAPERASAPG---GRLAEVCTVLLRGDEL 78  
DB 101 ODIISQRCICGHIKIRRLRSGLFNKIKLQIRISILGSGTSGIYADVPAQVGLDEL 160  
OY 79 EOIRPSVYRNVARQL-----HIPLOSEPVTDAFLAVAGHIFSGATMGVSLYSV 130  
DB 161 ERNHPRIYNGVARQICRNPGGEHTP---DAVSLILGAGRELFRVEITWSVLSIFAI 216  
OY 131 AAGLAVCYROAPAMVHALVDCIGFVRKTLATWLRRCGW---TDVLKCVSTDPGF 186  
DB 217 AGSLSDVCYRQGHPEYLPKLMESVYEIDELVPMINENCGSGINTHVLPNTSLNP-- 274  
OY 187 RSHWLVAITL-CSRG-----RFLKAFFLLPE 212  
DB 275 -LEMTLVIGVGFGLLVEMILFRIFNLIVPK 305

## RESULT 10

ID 09V612 PRELIMINARY; PRT; 247 AA.  
AC 09V612;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE CG8238 protein.  
GN BUFFY OR CG8238.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RA MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sultun G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Chame M., Pfeiffer B.D.,  
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,  
RA Abril J.F., Agbayan A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeter F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh K.-F., Zaveri J.S., Zhan M., Zhang X., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of Drosophila melanogaster".  
RL Science 287:2185-2195(2000).  
DR EMBL: AE003825; AAF58628.1;  
DR HSSP: 007817; 1MA2.  
DR FLYBase: FBgn0040491; Buffy.  
DR InterPro: IPR000712; BCL2\_BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam: PF00452; BCL-2; 1.  
DR SMART: SM00337; BCL; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
SO SEQUENCE 247 AA; 27466 MW; A2C4325AF4C1620 CRC64;

Query Match 21.4%; Score 234; DB 5; Length 247;  
Best Local Similarity 33.3%; Pred. No. 9e-13;  
Matches 54; Conservative 29; Mismatches 61; Indels 18; Gaps 4;

OY 25 KELVAQAKALGREYVHARLLRAGL--SMSAPERASPARC---GRLAEVCTVLLRLGDEL 78  
DB 87 QDIISGRLCGHYTKRRRLRSGLNKKLGRLGRLSILGTSMGIVRDVFPAYVYLGDEL 146  
OY 79 EOIRSVYRNVAROL-----HIPLQSEPVYDAFLAVAGHIFSAGITWGVSLYSV 130  
DB 147 EHMHRITNGVARQJCRNPGSEFHP---DAVSLLGAVGHELRVETWTSKVISLRF 202  
OY 131 AAGLAVDCVROAPMAVHALVDCLEFVRKTLATMLRRRGW 172  
DB 203 AGGLSVDCVROGHPYLPKLMSEVEIDELVPMINENGW 244

RESULT 11

ID Q95083 PRELIMINARY; PRT; 317 AA.

AC Q95083;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE GH01265P  
GN DEBCL OR CG12397.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RA Stapleton M., Brockstein P., Hong L., Abmayan A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Fiske E., George R.,  
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY058249; AAL13478.1;  
DR FLYBase: FBgn0029131; debcl.  
DR InterPro: IPR000712; BCL2\_BH.  
DR Pfam: PF00452; BCL-2; 1.  
DR SMART: SM00337; BCL; 1.  
SO SEQUENCE 317 AA; 34649 MW; 46B22FED1CC6F01F CRC64;

Query Match 19.5%; Score 213.5; DB 5; Length 317;  
Best Local Similarity 35.0%; Pred. No. 7.7e-11;  
Matches 55; Conservative 28; Mismatches 63; Indels 11; Gaps 5;

OY 26 ELVQAQAKALGREYVHARLLRAG-LSWSAPER---ASPARGRLAECVTLRLGDELQ 80  
DB 96 DINDGKCLCGYTRARLRAGVLRKYÖRLRNILDPSSHVIVEVPALMSGEELER 155  
OY 81 IRPSYRNVAROL-HIP---LQSEPVYDAFLAVAGHIFSAGITWGVSLYSVAGLAV 136  
DB 156 MHRVYTNISQLSRAPGELSDMAMMLNLVAKDLFRSSITWGTIISIFAVCGFAI 215

OY 137 DCVROAPMAVHALVDCLEFVRK--TLATWLRRRG 171  
DB 216 DCVROGHEFDQLDGLDGLAEIRGRLLADRRRWG 252

RESULT 12

ID Q35843 PRELIMINARY; PRT; 235 AA.

AC Q35843;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Bcl-x-gamma.  
GN BCL2L.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-B6/CBA; TISSUE=THYMUS;  
RX MEDLINE=98051053; PubMed=9390687;  
RA Yang X.-F., Weber G.F., Cantor H.;  
RT "A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells".  
RL Immunity 7:629-639(1997).  
DR EMBL: U51277; AAC53458.1;  
DR HSSP: P53563; 1AF3.  
DR MGD: MGI:88139; Bcl2l.  
DR InterPro: IPR000712; BCL2\_BH.  
DR InterPro: IPR001093; BCL2\_BH.  
DR InterPro: IPR002475; BCL2\_BH4.  
DR InterPro: IPR004725; BCL2\_reg.  
DR Pfam: PF00452; BCL-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART: SM00337; BCL; 1.  
DR SMART: SM00265; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01259; BH3; 1.  
DR PROSITE: PS01260; BH4; 1;  
DR PROSITE: PS00603; BH4-2; 1.  
DR PROSITE: PS50063; BH4-2; 1.  
SO SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;

Query Match 14.5%; Score 159; DB 11; Length 235;  
Best Local Similarity 22.3%; Pred. No. 3.3e-06;  
Matches 52; Conservative 31; Mismatches 80; Indels 70; Gaps 8;

OY 21 SPTDKELVAQAKALREYVHARLLRAGLSMS-----APERA----- 56  
DB 2 SOSNRELV-----DFLSYKLSOKGYSMSOFSVDEENREAPETAERTPSAINGN 54  
OY 57 -----SPAPGR-----LAECVTLRLGDELQIRSVYRNVAROLHI 95  
DB 55 PSMHLADSPAVNGATGHSSSLDAREYIPAAVAKQALREAGDFELRYRRAESDLSQHI 114  
OY 96 PLQSEPVYDAFLAVAGHIFSAGITWGVSLYSVAGLAVDCVROAPMAVHALVDCIG 155  
DB 115 ---TGTAVQSEFQVYNELFRGVNMGRIVAFFSGALCVESVKEQVLSRLASMA 171  
OY 156 EFKRTLATWLRRRGW-----TDVLKCVSTDPGFRSH-----WLVAT 194  
DB 172 TYLNLHLEPFIQENGWGVSGTPLRSYFRRLVY-PVAAEHVCDPSLMEVET 223

RESULT 13

ID Q923R6 PRELIMINARY; PRT; 236 AA.

AC Q923R6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE B-cell lymphoma protein 2.  
GN BCL2.  
OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
NCBI\_TaxID=10030;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Lai D.Z., Chen W., Wang H.T.;  
RT "Construction of a robust CHO cell line for biopharmaceutical use."  
RL Submitted (JUL-2001) to EMBL/GenBank/DBJ databases.  
DR EMBL; AF404339; AAK92201.1; -  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH4.  
DR InterPro: IPR002475; Bcl2\_family.  
DR InterPro: IPR004725; Bcl2\_reg.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
DR PROSITE: PS01259; BH3; UNKNOWN\_1.  
DR PROSITE: PS01260; BH4\_1; UNKNOWN\_1.  
DR PROSITE: PS50063; BH4\_2; 1.  
SQ SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;  
  
Query Match 14.2%; Score 155; DB 11; Length 236;  
Best Local Similarity 21.8%; Pred. No. 7.5e-06;  
Matches 47; Conservative 35; Mismatches 78; Indels 56; Gaps 7;  
  
OY 28 VQAQAKALG-----REYHARLLRAGLSW-----SAPERASPAAG-----QIHT-P 96  
DB 1 MAQAGRTGYDNREIVMKYHYKLSQSGYEMDGDVDAALPGAAPPTGISFQPSNPTRA 60  
OY 62 -----GRLAEVCTVLLRLGDELEQIRPSYRNVAR-----QIHT-P 96  
DB 61 VHRDMAKRSPLRPVATGPTLSPVPYVHLTLRRAGDPSRRYRDFAEMSSQLHLP 120  
OY 97 LOSEPVTDAFLVAGHIFSAGITWGKVVSLYSVAGLAVDCVROAQPAMVHALVDCIG 156  
DB 121 FTRK-----GRFAIVDEELPRDGVNMGRIYAFPFEGGVMEVSEVNSPLVDNALMTE 176  
OY 157 FVAKTLATWLLRRRGWTDVLCV-VSTDPGFRSHWL 191  
DB 177 YLNRHLHTWIIQDNGGMDAFELVGPVRLPDEFSL 212  
  
RESULT 14  
OQOMX2 PRELIMINARY; PRT; 188 AA.  
AC OQOMX2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Bcl-x (Fragment).  
GN BCL2L.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA MEDLINE:20350651; PubMed:10894153;  
RX Rucker E.B. III, Dietisseau P., Wagner K.U., Garrett L.,  
RT Wyszewski B., Flaws J.A., Hennighausen L.,  
RT "Bcl-x and Bax regulate mouse primordial germ cell survival and  
apoptosis during embryogenesis."  
RL Mol. Endocrinol. 14:1038-1052(2000).  
DR EMBL; AF088904; AAC72232.1; -  
DR HSSP; P53563; IAF3.  
DR MGD; MGI:88139; Bcl2L.

DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH4.  
DR InterPro: IPR002475; Bcl2\_family.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01259; BH3; 1.  
DR PROSITE: PS01260; BH4\_1; 1.  
DR PROSITE: PS50063; BH4\_2; 1.  
FT NON\_TER 188  
SQ SEQUENCE 188 AA; 21126 MW; 4E62F8356D248E52 CRC64;  
  
Query Match 14.1%; Score 154.5; DB 11; Length 188;  
Best Local Similarity 22.3%; Pred. No. 6.3e-06;  
Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;  
  
OY 21 SPDKELVQAQKALGREYHARLLRAGLSWS-----APERA----- 56  
DB 2 SQSNRELIV-----DFLSYKLSQSGYSMSQSDVEENRTAPEDEARETPSAINGN 54  
OY 57 -----SPAAGR-----LAEVCTVLLRLGDELEQIRPSYRNVARQLHI 95  
DB 55 PSWHLADSPAVNGATGSHSSLDAREVIYPMAYKQALREAGDEFEELRYRRAFSDLTSQLHI 114  
OY 96 PLQSEPVYDAFLVAGHIFSAGITWGKVVSLYSVAGLAVDCVROAQPAMVHALVDCIG 155  
DB 115 ---TPGTAVQSEFQVAVNEELPRDGVNMGRIYAFPSFGALCVSEVDKEMOVLASRIASWMA 171  
OY 156 EFVRKTLATWLLRRRGW 172  
DB 172 TYINDHLEPWIQENGW 188  
  
RESULT 15  
O35844 PRELIMINARY; PRT; 233 AA.  
AC O35844;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Bcl-xL.  
GN BCL2L.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA STRAIN-B6/CBA; TISSUE=THYMUS;  
RX MEDLINE:98051053; PubMed:9390687;  
RT Yang X.-F., Weber G.F., Cantor H.,  
RT "A novel Bcl-x isoform connected to the T cell receptor regulates  
apoptosis in T cells."  
RL Immunity 7:629-639(1997).  
DR EMBL; U51278; AAC53459.1; -  
DR HSSP; P53563; IAF3.  
DR MGD; MGI:88139; Bcl2L.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH4.  
DR InterPro: IPR002475; Bcl2\_family.  
DR InterPro: IPR004725; Bcl2\_reg.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01258; BH2; 1.  
DR PROSITE: PS01259; BH3; 1.

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DR PROSITE; PS01260; BH4_1; 1.  
DR PROSITE; PSS0063; BH4_2; 1.  
SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;
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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 7.50783 Seconds

(without alignments)  
1176.699 Million cell updates/sec

Title: US-09-682-667-2

Perfect score: 1094

Sequence: 1 MEVLRSSVFAEIMDAFDR.....TLCSPGRFIKAFLLPER 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164.5	15.0	236	1 BCL2_RAT	P49950 ratu
2	161.5	14.8	229	1 BCL2_BOVIN	002718 bos
3	156.5	14.3	236	1 BCL2_CRITO	093178 cric
4	154.5	14.1	233	1 BCLX_MOUSE	064373 mus
5	154.5	14.1	233	1 BCLX_MOUSE	P53563 ratu
6	154.5	14.1	236	1 BCL2_MOUSE	P10417 mus
7	152.5	13.9	228	1 ARL_XENLA	091827 xen
8	152.5	13.9	233	1 BCL2_CHICK	000709 gall
9	150.5	13.8	233	1 BCLX_HUMAN	007817 hom
10	150.5	13.8	233	1 BCLX_PIG	077737 sus
11	150.5	13.8	239	1 BCL2_HUMAN	P10415 hom
12	149.5	13.7	218	1 BAXB_HUMAN	007814 hom
13	144.5	13.2	192	1 BAXA_HUMAN	007812 hom
14	141.5	12.9	229	1 BCLX_CHICK	007816 gall
15	139.5	12.8	204	1 ARL1_XENLA	091828 xen
16	136	12.4	208	1 BAX_MOUSE	008734 mus
17	135.5	12.4	193	1 BCLM_MOUSE	P70345 mus
18	134.5	12.3	192	1 BAXA_BOVIN	002703 bos
19	132	12.1	211	1 BAK_HUMAN	016611 hom
20	131.5	12.0	193	1 BCLM_HUMAN	092843 hom
21	130.5	11.9	192	1 BAXA_MOUSE	063690 ratu
22	130.5	11.9	192	1 BAXA_MOUSE	063690 ratu
23	127	11.6	211	1 BAX2_HUMAN	013014 hom
24	117	10.7	350	1 MCL1_HUMAN	007820 hom
25	111.5	10.2	143	1 BAXD_HUMAN	P55269 hom
26	93.5	8.5	172	1 BFL1_MOUSE	007440 mus
27	93.5	8.5	115	1 CARB_MYCTU	P57689 myc
28	92.5	8.5	175	1 BFL1_HUMAN	016548 hom
29	84.5	7.7	672	1 ACSA_PHYBL	001562 phy
30	84.5	7.7	1121	1 CARB_MYCLE	090332 myc
31	84	7.7	177	1 NR13_COTJA	090343 cotu
32	83	7.6	941	1 DNAB_RHOMR	030477 rho
33	82	7.5	551	1 SMA4_MOUSE	P97471 mus

34	82	7.5	552	1 SMA4_HUMAN	013485 hom
35	82	7.5	552	1 SMA4_PIG	090439 sus
36	82	7.5	552	1 SMA4_RAT	070437 ratu
37	81.5	7.4	311	1 PCAO_AGR5	P52668 agri
38	81	7.4	1081	1 CARB_SYNY3	055756 syn
39	80.5	7.4	2003	1 NTC4_HUMAN	094466 hom
40	79.5	7.3	406	1 WCAL_SALTY	P26388 salm
41	79	7.2	205	1 GTSL_ASCSU	P46436 asca
42	79	7.2	312	1 MTA_SPRCO	069967 stre
43	78	7.1	501	1 CP2B_RAT	035132 ratu
44	77.5	7.1	319	1 MOCB_STNP7	056208 syn
45	77.5	7.1	385	1 RURE_PSEOL	P17052 pseud

## ALIGNMENTS

RESULT 1	BCL2_RAT	STANDARD;	PRT;	236 AA.
AC	P49950: 062837; 064032;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Apoptosis regulator Bcl-2.			
GN	BCL2 OR BCL-2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=94193015; PubMed=8144041;			
RA	Sato T., Irie S., Krajewski S., Reed J.C.;			
RT	"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";			
RL	Gene 140:291-292(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Ovary;			
RX	MEDLINE=95129487; PubMed=7828536;			
RA	Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;			
RT	"Expression of members of the bcl-2 gene family in the immature rat			
RT	ovary: equine chorionic gonadotropin-mediated inhibition of granulosa			
RT	cell apoptosis is associated with decreased bax and constitutive			
RT	bcl-2 and bcl-xlong messenger ribonucleic acid levels.";			
RL	Endocrinology 136:232-241(1995).			
RN	[3]			
RP	SEQUENCE OF 19-172 FROM N.A.			
RX	MEDLINE=95059917; PubMed=7969891;			
RA	Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,			
RA	Lindholm D.;			
RT	"bcl-2 messenger RNA is localized in neurons of the developing and			
RT	adult rat brain.";			
RL	Neuroscience 61:165-177(1994).			
CC	-1- FUNCTION: Suppresses apoptosis in a variety of cell systems			
CC	including factor-dependent lymphohematopoietic and neural cells.			
CC	Regulates cell death by controlling the mitochondrial membrane			
CC	permeability. Appears to function in a feedback loop system with			
CC	caspases. Inhibits caspase activity either by preventing the			
CC	release of cytochrome c from the mitochondria and/or by binding to			
CC	the apoptosis-activating factor (APAF-1).			
CC	-1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and			
CC	Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2			
CC	domains, and is necessary for anti-apoptotic activity (By			
CC	similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular			
CC	membrane of the nuclear envelope and the endoplasmic reticulum.			
CC	-1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with			
CC	highest levels in reproductive tissues. In the adult brain,			
CC	expression is localized in mitral cells of the olfactory bulb,			
CC	granule and pyramidal neurons of hippocampus, pontine nuclei,			
CC	cerebellar granule neurons, and in ependymal cells. In prenatal			

```

CC brain, expression is higher and localized in the neuroepithelium
CC and in the cortical plate.
CC - DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC - PWM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC - PWM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC - SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L14680; AAA53662.1; -
DR EMBL: U34964; AAA75687.1; -
DR HSSP: 007817; 1MAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FW DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT CONFLICT 42 42 A -> R (IN REF. 2).
FT CONFLICT 157 157 E -> G (IN REF. 1).
FT CONFLICT 164 164 S -> Y (IN REF. 2).
FT CONFLICT 212 212 L -> Q (IN REF. 2).
SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

Query Match 15.0%; Score 164.5; DB 1: Length 236;
Best Local Similarity 23.3%; Freq. No. 8e-08; Mismatches 79; Indels 57; Gaps 8;
Matches 52; Conservative 35;

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OY 97 LQSEPVTDFAFLAVAGHIFPSAGITWGVSLYSVAGLAVDCVROAQPAMVHALVDCGE 156
DB 121 FPAR-----GRAFTVVEELFRDGVNMGRIVAFEPFGVGVESVNMESLVDNIALMNT 176
OY 157 EVRKTLATWLRRRGWTDLKCV-VSTDGFRSHW-VATLCS 197
DB 177 YLNRHLHTWIDONGDAVEELGFSMRPLDFEWSLSTKLTS 219

RESULT 2
BCL2_BOVIN
ID BCL2_BOVIN STANDARD; PRT; 229 AA.
AC 002718;
DR 16-OCT-2001 (Rel. 40, Created)
DR 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Thymus;
RA Reyes R.A., Cockrell G.L.;
RT "Bovine leukemia virus associated leukemogenesis is correlated
RT with suppression of programmed cell death and increased expression
RT of Bcl-2."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC - SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC - SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum (By
CC similarity).
CC - DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC - PWM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated
CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
CC similarity).
CC - PWM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC - SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

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CC -----
DR EMBL: U92434; AAB53319.1; -.
DR HSSP: C07817; 1MA2.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10 30 BH4.
FT DOMAIN 64 68 POLY-PRO.
FT DOMAIN 69 72 POLY-ALA.
FT DOMAIN 83 97 BH3.
FT DOMAIN 126 145 BH1.
FT DOMAIN 177 192 BH2.
FT TRANSMEM 202 223 POTENTIAL.
FT SITES 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 229 AA; 25099 MW; ADIDDAF96FFFIID CRC64;

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Query Match      14.8%; Score 161.5; DB 1; Length 229;
Best Local Similarity 23.1%; Pred. No. 1.4e-07;
Matches 49; Conservative 35; Mismatches 77; Indels 51; Gaps 7;

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QY 37 EYVHARILRAGLSW-----SAPERASPPG-----GLAE----- 66
DB 17 KVIHKLISRGYEMDAGDGAAPGAPGAPGILSSQGPRTAPSPRTSPPPPPAAAGAPAP 76
QY 67 -----VCTVLLRLGDELBOIRPSYRVNAROLHI-PLQSEPVYNDAPLAVAGHIPSGI 119
DB 77 SEVPPVYVHILTRQAGDDFERRRRRDPFAEMSSQHLTFPTAR-----ERFATVVEELFRDGV 132
QY 120 TWGKVVSLIXSVAGLAVDVCVROAQPAMVAHVDLCEFYRKTLATWLRRRGWTDLKCV 179
DB 133 NMGRIYAFEEFGVCKVESVNRMSPLVDISIALMTEYINRLHWTIQNGMDARVELY 192
QY 180 -VSTDGFRSHMLVATLCSFGRPLKAAFFLL 210
DB 193 GPMRPLDFESWL-----SLKALLSLAL 215

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RESULT 3
BCL2_CRILLO
ID BCL2_CRILLO STANDARD; PRT; 236 AA.
AC Q9JTV8;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Citellus longicaudatus (long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_Taxid=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=20431763; PubMed=10973819;
RA Tomicic M.T.; Christman M.; Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
  protein.";
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).

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RN [2]
RP SEQUENCE FROM N.A.; AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=11181062;
RA Tomicic M.T.; Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
  and caspase-3.";
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
  including factor-dependent lymphohematopoietic and neural cells.
  Regulates cell death by controlling the mitochondrial membrane
  permeability. Appears to function in a feedback loop system with
  caspases. Inhibits caspase activity either by preventing the
  release of cytochrome c from the mitochondria and/or by binding to
  the apoptosis-activating factor (APAF-1) (By similarity).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and
  Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
  domains, and is necessary for anti-apoptotic activity (By
  similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
  membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
  for interaction with RAF-1 (By similarity).
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
  anti-apoptotic activity. Growth factor-stimulated phosphorylation
  on Ser-70 by PKC is required for the anti-apoptosis activity and
  occurs during the G2/M phase of the cell cycle (By similarity). In
  the absence of growth factors, Bcl2 appears to be phosphorylated
  by other protein kinases such as ERKs and stress-activated kinases
  (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
  (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
  cleaved protein, lacking the BH4 domain, has pro-apoptotic
  activity, causes the release of cytochrome c into the cytosol
  promoting further caspase activity.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ271720; CAB92245.1; -.
DR HSSP: C07817; 1MA2.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 64 68 POLY-PRO.
FT DOMAIN 69 72 POLY-ALA.
FT DOMAIN 83 97 BH3.
FT DOMAIN 126 145 BH1.
FT TRANSMEM 202 223 POTENTIAL.
FT SITES 34 35 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT MOD_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

```

SQ SEQUENCE 236 AA: 26491 MW: BECADFIEF337228 CRC64:  
 Query Match 14.3%; Score 156.5; DB 1; Length 236;  
 Best Local Similarity 22.4%; Pred. No. 4.2e-07;  
 Matches 50; Conservative 36; Mismatches 80; Indels 57; Gaps 8;  
 OY 28 VAQAALG-----REYHARLLRAGLSW-----SAPERASPAAG-----OLHI-P 61  
 DB 1 MAQAGRTGDNREIYMKIHYLSQREMDVDYDAAPLGAAPPGIFSPQESNPPPA 60  
 OY 62 -----GRLAECYVLLRLGDELEQIRPSYRNVAR-----OLHI-P 96  
 DB 61 VARDMAARTSPRLRPVATTPGTPSPVPHLTIRAGDEFSRRTRRDPFAEMSSQLHLTP 120  
 OY 97 LOSEPVTDAFLAVAGHIFSGATGWKVSLSVAAGLAVDCVROAQPAMVHALVDCLOE 156  
 DB 121 FTAR-----GRTAVVEELFRDGVNMGRIAYAFEPFGVMCEVSVMEMSLVIALMMTE 176  
 OY 157 FVRKTLATMLRRGGMTDYLKCV-VSTDGFRSHWL-VATLCS 197  
 DB 177 YLNRHLHTWIDNGMDAFVELYGPSVRLEFDFSMLSLTLIS 219  
 RESULT 4  
 BCLX\_MOUSE STANDARD: PRT: 233 AA.  
 ID BCLX\_MOUSE 064373: 060657: 060658: 061338:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-2A4B;  
 RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;  
 RL Submitted (Mar-1995) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RN SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).  
 RC STRAIN-C57BL/6; TISSUE-Brain;  
 RX MEDLINE=9531139; PubMed=7607090;  
 RA Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,  
 RT Thompson C.B., Nunez G.;  
 RT "bcl-xL is the major bcl-x mRNA form expressed during murine  
 RL development and its product localizes to mitochondria.";  
 RL Development 120:3033-3042(1994).  
 RN (3)  
 RN SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).  
 RC TISSUE-Pre-B cell;  
 RX MEDLINE=95052604; PubMed=7963517;  
 RA Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;  
 RT "Cloning and molecular characterization of mouse bcl-x in B and T  
 RT lymphocytes.";  
 RL J. Immunol. 153:4388-4398(1994).  
 RN (4)  
 RN SEQUENCE FROM N.A. (ISOFORM X(BETA)).  
 RC STRAIN-C57BL/6 X CBA; TISSUE-Thymus;  
 RX MEDLINE=98051053; PubMed=9390687;  
 RA Yang X.-F., Weber G.F., Cantor H.;  
 RT "A novel bcl-x isoform connected to the T cell receptor regulates  
 RT apoptosis in T cells.";  
 RL Immunity 7:629-639(1997).  
 RN (5)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=97289584; PubMed=9144489;  
 RA Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,  
 RA Ohba S., Seidman M.F., Nunez G.;  
 RT "Genomic organization, promoter region analysis, and chromosome  
 RT localization of the mouse bcl-x gene.";

RL J. Immunol. 158:4750-4757(1997).  
 CC -I- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S)  
 CC isoform promotes apoptosis.  
 CC -I- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).  
 CC -I- ALTERNATIVE PRODUCTS: 4 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S),  
 CC BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -I- TISSUE SPECIFICITY: WIDELY EXPRESSED. WITH HIGHEST LEVELS IN THE  
 CC BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-  
 CC TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN  
 CC ACTIVATED.  
 CC -I- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND  
 CC POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN  
 CC POSTNATAL TISSUES.  
 CC -I- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -I- PTM: Proteolytically cleaved by caspases during apoptosis (By  
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
 CC apoptotic activity (By similarity).  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X83574: CAA58557.1; -;  
 DR EMBL: L35049: AAA51039.1; -;  
 DR EMBL: L35048: AAA51040.1; -;  
 DR EMBL: U10102: AAA82174.1; -;  
 DR EMBL: U10101: AAA82173.1; -;  
 DR EMBL: U10100: AAA82172.1; -;  
 DR EMBL: U51279: AAC53460.1; -;  
 DR EMBL: U78031: AAB96881.1; -;  
 DR EMBL: U78030: AAB96881.1; JOINED.  
 DR HSSP: P53563: IAF3.  
 DR MGD: MGI:88139; Bcl2L1.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR000393; BCL2\_BH4.  
 DR InterPro: IPR004725; Bcl2-reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS01260; BH4\_2; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 FT Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.

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FT TRANSMEM 210 226 POTENTIAL.
FT VASPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).
FT VASPLIC 189 233 DFFVLYGNNAAESRKGQERNRWELTGMVAGVLLGSL
FT VASPLIC 194 233 FSRK -> VRTTPLYCPLACVSLICERP (IN ISOFORM
FT VASPLIC 194 233 BCL-X(BETA)).
FT VASPLIC 194 233 LYGNNAAESRKGQERNRWELTGMVAGVLLGSLFSRK
FT VASPLIC 194 233 -> GHDCMCGSAGLLTLOSEVTRH (IN ISOFORM BCL-
FT VASPLIC 194 233 X(DELTA-TM)).
SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CMC64;

Query Match 14.1%; Score 154.5; DB 1; Length 233;
Best Local Similarity 22.3%; Pred. NO. 6.3e-07;
Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;

QY 21 SPTDELVAQAKALGREVYHARLLRAGLSMS-----APEPA----- 56
DB 2 SOSNRELVV-----DFLSYRLSOKGYWSQFSDVEENRTPEETEARETPSAIGN 54
QY 57 -----SPAPGCR-----LAECVTLLRLGDELLEQIRPSVYNNVARQLHI 95
DB 55 PSWMHLADSPAVNGATGCHSSSLDAREVIPAAMAKALREAGDEFLRYRAFDLSQLHI 114
QY 96 PLOSEPVTDAFLAVAGHIFSGAGITGWKYSLSVAAGLAVDCVRQAPAMVHALVDCIG 155
DB 115 --TFGTAYQSEFEQYVNEFLFDGVNMGRIVAFSEFGALCVESVDKEMQVLVSRIASMA 171
QY 156 EFVVRTLATWLRRRGGW 172
DB 172 TYLNDHLEPWIQENGW 188

RESULT 5
ID BCLX_RAT STANDARD: PRT: 233 AA
AC P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
BT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BLC2L OR BCLX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC TISSUE-Brain;
RA Michaelidis T.M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Wesselingh S.L., David G.L., Choi S., Veltona M., Hardwick J.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC TISSUE-Thymus;
RA MEDLINE=96278736; PubMed=8662675;
RA Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT unspliced RNA, promotes apoptosis in promyeloid cells.";
RN J. Biol. Chem. 271:13258-13265(1996).
RN 14
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC STRAIN-Sprague-Dawley; TISSUE-Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RN Endocrinology 136:232-241(1995).
RN 15

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RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=98010630; PubMed=9346936;
RA Arlotom M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA Morikawa K.;
RT "Crystal structure of rat Bcl-xL. Implications for the function of
RT the Bcl-2 protein family.";
RL J. Biol. Chem. 272:27886-27892(1997).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and
CC Bcl-x(beta) isoforms promote apoptosis.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)
CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC DETECTABLE LEVEL OF BCL-X(S).
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X82537; CAA57886.1; -
DR EMBL: X82537; CAA57887.1; -
DR EMBL: U10579; AAA19257.1; -
DR EMBL: U72350; AAB17353.1; -
DR EMBL: U72349; AAB17352.1; -
DR EMBL: U34963; AAA77686.1; -
DR EMBL: S76513; AAC60701.1; ALT_INIT.
DR EMBL: S78284; AAC60702.1; -
DR PDB: 1AF3; 07-JUL-97.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW 3d-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.

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KM Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;  
 KM Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD.RES 70 70 PHOSPHORYLATION (BY PTC).  
 FT VARSPPLIC 193 236 DAFVELGFSMRPLEDFSLSKTLLSLALVACITLGLAYL  
 FT GHK -> VGACTIVE (IN ISOFORM BETA).  
 SQ SEQUENCE 236 AA; 26425 MW; AAB5FE6B0766BE0A CRC64;  
 Query Match 14.1%; Score 154.5; DB 1; Length 236;  
 Best local similarity 22.4%; Pred. No. 6.4e-07;  
 Matches 50; Conservative 36; Mismatches 80; Indels 57; Gaps 8;  
 QY 28 VAOAKALG-----REYVHARLLRAGLSW-----SAPERASPARG----- 61  
 DB 1 MAQAGRTGYDNRREIVAKYIHYKLSRGYEMDAGDADAAPLGAAPFGIFSFPESNPMRA 60  
 QY 62 -----GRLAEVCTVLLRLGDELEQIRPSYRNVAR-----QHT-P 96  
 DB 61 VHEMARARSPRLPVAATGAPALSPVPCVHLTLRRAGDGSRRYRDRFAEMSSQLHLTP 120  
 QY 97 LOSEPVTDAFLAVAGHIFSAGITMGKVVSLYSVAAGLAEDCVRAQAPAMVHALVDCLE 156  
 DB 121 FAR-----GRFATVVEBELFRDGVNMGRIYAFEPFGVMCEVSNREMSPLVDIALMTE 176  
 QY 157 EVRKTLATWLRRRGWTDLKCV-VSTDGFSNHWL-VATLCS 197  
 DB 177 YINRHLHTWIDONGWDFAVELYGLSPMRPLDFSMILSKTLLS 219  
 RESULT 7  
 ARL\_XENLA  
 ID ARL\_XENLA STANDARD: PRT; 228 AA.  
 AC Q91827;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator R1 (XRL) (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Head;  
 RX MEDLINE=95331613; PubMed=7607538;  
 RA Cruz-Reyes J., Tata J.R.;  
 RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
 cell-survival genes.";  
 RL Gene 138:171-179(1995).  
 CC -1- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
 CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
 CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
 CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: X82462; CAA57845.1; .

DR HSP: C007817; 1MA2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR Pfam: PF0452; BCL-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR Apoptosis; Transmembrane.  
 FT NON\_TER 1 1  
 FT DOMAIN 120 139 BH1.  
 FT DOMAIN 171 186 BH2.  
 FT TRANSMEM 207 227 POTENTIAL.  
 SQ SEQUENCE 228 AA; 25068 MW; C499DA49A585F8A9 CRC64;  
 Query Match 13.9%; Score 152.5; DB 1; Length 228;  
 Best local similarity 23.7%; Pred. No. 9.3e-07;  
 Matches 40; Conservative 30; Mismatches 74; Indels 25; Gaps 5;  
 QY 20 RSPDKELVAQ-----AKALGREYVHARLLRAGLSWSAPERASPARGRLAEVC-- 68  
 DB 28 RGSPPDKYLTREGQWMAQSDGLSRALVEDLVRKYLQGRSL-----VPPSG--AASCAL 77  
 QY 69 -TYLRLGDELEQIRPSYRNVARQHLIPLOSEPVTDAFLAVAGHIFSAGITMGKVVSL 127  
 DB 78 HSMARAGDEFEFRQASSEISTQIHV--TPGTAVARPAEYAGSLFQGVNMGRIYAF 134  
 QY 128 YSAAGLAEDCVRAQAPAMVHALVDCLEGEVFRKTLATWLRRRGWTDLV 176  
 DB 135 FVFGAALCAESVKNKEMSPLLPRIQDMVWYLETENLFDWQSGNGMGFL 183  
 RESULT 8  
 BCL2\_CHICK  
 ID BCL2\_CHICK STANDARD: PRT; 233 AA.  
 AC Q00709;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-B-cell lymphoma;  
 RX MEDLINE=92379084; PubMed=1511008;  
 RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;  
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken  
 RT homologue of the Bcl-2 oncoprotein.";  
 RL Biochim. Biophys. Acta 1132:109-113(1992).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and



CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC Heterodimerization with BAX does not seem to be required for anti-  
 CC apoptotic activity.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS  
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING  
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING  
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.  
 CC -1- DOMAIN: The B4 domain is required for anti-apoptotic activity.  
 CC The B4 and B2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the B4 domain, has pro-apoptotic  
 CC activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: 223116; CAAB0662.1; -  
 CC EMBL: 223115; CAAB0661.1; -  
 CC EMBL: U72398; AAB17354.1; -  
 CC PDB: 1BXL; 29-OCT-97.  
 CC PDB: 1LXL; 21-APR-97.  
 CC PDB: 1MAZ; 21-APR-97.  
 CC Genew: HGNC:992; BCL2L1.  
 CC MIM: 600039; -  
 CC InterPro: IPR002475; BCL2\_family.  
 CC InterPro: IPR000712; Bcl2\_BH.  
 CC InterPro: IPR003093; Bcl2\_BH4.  
 CC InterPro: IPR004725; Bcl2\_reg.  
 CC Pfam: PF00452; Bcl-2; 1.  
 CC SMART: SM00337; BCL; 1.  
 CC SMART: SM00265; BH4; 1.  
 CC SMART: SM00337; BCL; 1.  
 CC TIGRfam: TIGR00865; bcl-2; 1.  
 CC PROSITE: PS50062; BCL2\_FAMILY; 1.  
 CC PROSITE: PS01080; BH1; 1.  
 CC PROSITE: PS01258; BH2; 1.  
 CC PROSITE: PS01259; BH3; 1.  
 CC PROSITE: PS01260; BH4\_1; 1.  
 CC PROSITE: PS50063; BH4\_2; 1.  
 CC Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 CC 3D-structure.  
 CC  
 CC FT DOMAIN 4 24 BH4.  
 CC FT DOMAIN 86 100 BH3.  
 CC FT DOMAIN 129 148 BH1.  
 CC FT DOMAIN 180 195 BH2.  
 CC FT TRANSMEM 210 226 POTENTIAL.  
 CC FT SITE 61 61 CLEAVAGE BY CASPASE-1.  
 CC FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 CC FT VARSPPLIC 189 233 DFEVLYGNNAAESRKGRENRFLTGMVAGVYLGSL  
 CC FT VARSPPLIC 189 233 FSRK -> VRTKPLVCPFLASGRSPFALLLYFLICWVI  
 CC FT MUTAGEN 61 61 D->A: NO CLEAVAGE BY CASPASE-1 NOR BY

FT MUTAGEN 131 133 CASPASE-3.  
 FT MUTAGEN 135 137 FRD->VRA: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 138 140 VAM->AIL: LOSS OF ANTI-APOPTOTIC  
 FT MUTAGEN 138 140 ACTIVITY.  
 FT MUTAGEN 138 140 GRI->ELN: LOSS OF ANTI-APOPTOTIC  
 FT MUTAGEN 138 140 ACTIVITY.  
 FT MUTAGEN 138 140 G->A: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 148 148 G->E: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 156 156 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT MUTAGEN 176 176 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT MUTAGEN 188 189 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY  
 FT MUTAGEN 189 189 BY ABOUT HALF.  
 FT MUTAGEN 189 189 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT CONFLICT 70 70 G -> A (IN REF. 1; CAAB0661).  
 SO SEQUENCE 233 AA: 26049 MM; E09D3CDD851AE3BE CRC64;  
 Query Match 13.8%; Score 150.5; DB 1; Length 233;  
 Best Local Similarity 22.3%; Pred. No. 1,4e-06;  
 Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;  
 QY 21 SPDKELVAQAKLAGREYHARLLRAGLSMS-----APER----- 56  
 DB 2 SOSNRELV-----DFLSYKLSQCKYSWSQSDVEENRTEADEGESMETPSAINGN 54  
 QY 57 -----SPAGGR-----LAECVTLRLGDELEQIRPSYRYNARQLHI 95  
 DB 55 PSMHLADSPAVNGVATGHSSSLDAREVIPAIAVQALREADEDEFELRRARAFSDLTSLHI 114  
 QY 96 PLOSEPVYTAFLAVAGHITSAGITGKVVSLYSVAAGLAVDCVQAQPMVAHALDCLG 155  
 DB 115 ---TPGTAYGSFQVYVNEFLRDGVNMGRIVAFESFGALCVESDKEMQVLVSRIAWMA 171  
 QY 156 EFVRKTATWLRRRGWM 172  
 DB 172 TYLNDHLEPWIOENGWM 188  
 RESULT 10  
 BCLX\_PIG STANDARD; PRT; 233 AA.  
 ID BCLX\_PIG  
 AC 077737;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUN-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCL2L OR BCLX.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99171363; PubMed=10072723;  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
 RT "Quantification of cardioprotective gene expression in porcine  
 RT short-term hibernating myocardium."  
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- DOMAIN: The B4 domain is required for anti-apoptotic activity.  
 CC The B4 and B2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By  
 CC similarity). The cleaved protein, lacking the B4 domain, has pro-  
 CC apoptotic activity (By similarity).







including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1 SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with Apaf-1 and Raf-1.  
 CC -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1 ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -1 TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1 DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with Raf-1.  
 CC -1 PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1 PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1 DISEASE: Involved in follicular lymphoma (FL) (also known as type  
 CC II chronic lymphocytic leukemia) by a chromosomal translocation  
 CC t(14;18)(q32;q21) which involves Bcl2 and Immunoglobulin gene  
 CC regions.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1 DATABASE: NAME=Atlas Genet. CytoGenet. Oncol. Haematol.;  
 CC WWW="http://www.infobiogen.fr/services/Chromancer/Genes/BCL2ID49.htm".  
 CC -----  
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 CC -----  
 CC EMBL: M13994; AAA51813.1; ALT\_SEQ.  
 CC EMBL: M13995; AAA51814.1; ALT\_SEQ.  
 CC EMBL: M14745; AAA35591.1; -  
 CC EMBL: X06487; CAA29778.1; -  
 CC EMBL: S72602; AAD14111.1; ALT\_SEQ.  
 CC PIR: A29409; TVHUA1.  
 CC PIR: B29409; TVHOB1.  
 CC PIR: A24428; TVHOB1.  
 CC PIR: C37332; C37332.  
 CC PIR: D37332; D37332.  
 CC HSSP: C07817; IMAZ.  
 CC Genew: HGNC:990; BCL2.  
 CC MIM: 151430; -  
 CC InterPro: IPR002475; BCL2\_family.  
 CC InterPro: IPR000712; BCL2\_BH.  
 CC InterPro: IPR003093; BCL2\_BH4.  
 CC InterPro: IPR004725; BCL2\_reg.  
 CC Pfam: PF00452; Bcl-2; 1.  
 CC Pfam: PF02180; BH4; 1.  
 CC SMART: SM00337; BCL; 1.  
 CC SMART: SM00265; BH4; 1.  
 CC TIGRFAMs: TIGR00865; bcl-2; 1.  
 CC PROSITE: PS50062; BCL2\_FAMILY; 1.  
 CC PROSITE: PS01080; BH1; 1.  
 CC PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;  
 KW Mitochondrion; Phosphorylation; Chromosomal translocation;  
 KW Polymorphism; Disease mutation.  
 FT DOMAIN 10 30  
 FT DOMAIN 93 107  
 FT DOMAIN 136 155  
 FT DOMAIN 187 202  
 FT TRANSMEM 212 233  
 FT SITE 34 35  
 FT MOD\_RES 70 70  
 FT VARSPIC 196 239  
 FT VARIANT 7 7  
 FT VARIANT 59 59  
 FT VARIANT 93 93  
 FT VARIANT 93 93  
 FT MUTAGEN 34 34  
 FT MUTAGEN 64 64  
 FT MUTAGEN 145 145  
 FT MUTAGEN 188 188  
 FT CONFLICT 48 48  
 FT CONFLICT 59 59  
 FT CONFLICT 117 117  
 FT CONFLICT 129 129  
 SO SEQUENCE 239 AA; 26266 MW; 3C49F2B71ADC9CB CRC64;  
 Query Match 13.8%; Score 150.5; DB 1; Length 239;  
 Best Local Similarity 21.9%; Pred. No. 1.5e-06;  
 Matches 46; Conservative 36; Mismatches 75; Indels 53; Gaps 7;  
 QY 37 EYVHARLRLAGLSM-----SAPERASPPAG-----GRLEAECT-- 69  
 DB 17 KYTHVRLSQRGYEMDAGVGAAPGAPGAPGIRSSPGHTPHPAASRDPAKTSPLQTPA 76  
 QY 70 -----VLRLGDELEQIRPSVYRNVAQLHI-PLQSEPVYTDATFLA 109  
 DB 77 APCAAGPALSPVPVPHVHLTRQAGDFSRRYRDRDAEMSSQHLTPFAR----GRFAT 132  
 QY 110 VAGHFSAGITWCKVYSLYSVAAGLAVDCYRQAPMAVHALVDCLEFVKRTLATLRRR 169  
 DB 133 VVEELFRDGVNMGRIYAFEEFGVGCVESSYRMSPLVDNIALMTYELNRHLHTWIDON 192  
 QY 170 GGTWDLKCV-VSTDPGFSHML-VATFCS 197  
 DB 193 GWDARFVELYGPMSRPLDFDSWLSKTLUS 222  
 RESULT 12  
 BAXB\_HUMAN  
 ID BAXB\_HUMAN STANDARD; PRT; 218 AA.  
 AC 007814;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, cytoplasmic isoform beta.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RX MEDLINE=93364978; PubMed=8358790;

```

RA Oliva 2.N., Millman C.L., Korsmeyer S.J.:  

RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  

RL accelerates programmed cell death.";  

CC Cell 74:609-619(1993).  

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  

CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS  

CC HOMOLOG E1B 19K PROTEIN.  

CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  

CC E1B 19K PROTEIN, BCL-X(L), MCL-1, AND A1.  

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  

CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  

CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  

CC ALTERNATIVE SPLICING.  

CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  

CC -1- DOMAIN: INTERACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  

CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  

CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  

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CC -----  

DR EMBL: L22474; AAA03620.1; -.  

DR PIR: B47538, B47538.  

DR HSSP: O07817; IMAZ.  

DR Genew: HGNC:959; BAX.  

DR MIM: 600040; -.  

DR InterPro: IPR002475; BCL2_family.  

DR InterPro: IPR000712; BCL2_BH.  

DR Pfam: PF00452; Bcl-2; 1.  

DR SMART: SM00337; BCL.1.  

DR PROSITE: PS01080; BH1; 1.  

DR PROSITE: PS01258; BH2; 1.  

DR PROSITE: PS01259; BH3; 1.  

DR PROSITE: PS50062; BCL2_FAMILY; 1.  

DR Apoptosis: Alternative splicing.  

FT DOMAIN 59 73 BH3.  

FT DOMAIN 98 118 BH1.  

FT DOMAIN 150 165 BH2.  

SQ SEQUENCE 218 AA; 24220 MW; F69DCD70F960192P CRC64;  

  

Query March 13.7%; Score 149.5; DB 1; Length 218;  

Best local similarity 28.8%; Pred. No. 1.6e-06;  

Matches 46; Conservative 29; Mismatches 72; Indels 13; Gaps 6;  

  

QY 22 PTDKELVAQAALGRE-VYHARLLRAGLSWSAPERA-SPAP-GGRLAECVTLRLGDEL 78  

DB 13 PTSSQIWKGTALLGFIODRAGRMG--GEAPELALDPVPODASTKRLSECKRIGDEL 70  

QY 79 EQIRSVYRNVARQRLHILOSEPVTYDIAFLAVAGIIFSNAG-ITWGKVVSLSYAAGLAVD 137  

DB 71 DS-----NNELDQMAIYADTDSREVEFFRVAADMFSGDNFMNMGVAALEFYFAKSLVK 123  

QY 138 CVYQAPAMVHALVDLGEFVRKTLATLRRRGGTVDYIK 177  

DB 124 ALCTKVPDLITFMGTIDFLERLLGNIGIODGGVRLIK 163  

  

RESULT 13  

ID BAXA_HUMAN STANDARD: PRT; 192 AA.  

AC 007812;  

FT 01-FEB-1995 (Rel. 31, Created)  

FT 01-FEB-1995 (Rel. 31, Last sequence update)  

DT

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15-JUN-2002 (Rel. 41, Last annotation update)  
Apoptosis regulator BAX, membrane isoform alpha.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_Taxid=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE-B-cell;  
MEDLINE=93364978; Pubmed=8358790;  
Olvera Z.N., Millman C.L., Korsmeyer S.J.;  
"Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
accelerates programmed cell death.";  
Cell 74:609-619(1993).  
[2]  
MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.  
MEDLINE=96091131; Pubmed=8521816;  
Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,  
Elangovan B., Chinnadurai G., Lutz R.J.;  
"A conserved domain in Bax, distinct from Bhl and Bh2, mediates cell  
death and protein binding functions.";  
EMBO J. 14:5589-5596(1995).  
[3]  
VARIANT PLASMACYTOMA GLU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC  
LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.  
MEDLINE=96200607; Pubmed=9531611;  
Meljertink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,  
Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;  
"Hematopoietic malignancies demonstrate loss-of-function mutations of  
Bax.";  
Blood 91:2991-2997(1998).  
-1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ANOGENOUS  
HOMOLOG ELB 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,  
ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.  
-1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
ELB 19K PROTEIN, BCL-X(L), MCL-1 AND A1.  
-1- SUBCELLULAR LOCATION: Membrane bound.  
-1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
ALTERNATIVE SPLICING.  
-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
-1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
-1- DISEASE: Defects in Bax are found in some cell lines from  
hematopoietic malignancies as T-cell acute lymphoblastic leukemia,  
Burkitt lymphoma, and plasmacytoma.  
-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL: L22473; AAA03619.1; -  
PIR: A47538; A47538.  
DR HSSP: Q07817; IMAZ.  
DR Genew: HGNC:959; BAX.  
DR MIM: 600040; -  
DR Interpro: IPR002475; BCL2\_family.  
DR Interpro: IPR000712; BCL2\_BH.  
DR Pfam: PF00452; BCL-2; 1.  
DR SMART: SM00357; BCL; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR



```
AC O91828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator B11 (XR11).
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RL cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X82461; CAA57844.1; -
DR HSSP: Q07817; 1MAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane.
KW DOMAIN
FT DOMAIN 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSMEM 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFC6BE6DDACA03 CRC64;

Query Match 12.8%; Score 139.5; DB 1; Length 204;
Best Local Similarity 26.2%; Pred. No. 1.2e-05;
Matches 28; Conservative 22; Mismatches 54; Indels 3; Gaps 1;

QY 66 EVCYVLLRLGDELEQIRSVYNNVARQLHIPLOSEPVTDAFLAVAGHIFSAGITGKVV 125
DB 57 EVLAQLLEATEEFELRYQRAFSDLTSLQHLI---TODTAAQSSRQYMGELFRGCTWGRIV 113
QY 126 SLISVAGLAVDCVRQAQPAWVHALVDCLGEFVRKTLATWLRRGW 172
DB 114 AFFSFGALCVESANKEMTDLPRIYQWVNVYLEHTLPWMQENCGW 160
```

Search completed: April 29, 2003, 11:23:54  
Job time : 9.50783 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 13.3473 Seconds

(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-2

Perfect score: 1094

Sequence: 1 MEVLRRSSVFSAEIMDAFDR.....TLCSPGRFLKAFAFULLPER 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	14.8	227	2 JE0203	apoptosis regulato
2	161.5	14.8	226	2 I53744	gene bcl-2 protein
3	157.5	14.4	216	2 B37332	transforming prote
4	156.5	14.3	236	2 JC7383	B-cell lymphoma 2
5	156	14.3	236	2 I67432	bcl-2 - rat (fragm
6	154.5	14.1	214	2 I49057	bcl-x transmembran
7	154.5	14.1	233	2 I49056	bcl-x long - mouse
8	154.5	14.1	236	1 TWMSA1	transforming prote
9	153.5	14.0	233	2 S51761	BCL-X protein - ra
10	152.5	13.9	233	2 A37332	transforming prote
11	151.5	13.8	199	1 TWMSB1	transforming prote
12	151.5	13.8	233	2 I67431	BCL-X-long - rat
13	150.5	13.8	233	2 B47537	apoptosis regulato
14	150.5	13.8	239	1 TVHU01	transforming prote
15	149.5	13.7	218	2 B47538	bcl-2-associated p
16	149	13.6	232	2 S24390	transforming prote
17	146.5	13.4	179	2 JC7255	Bax-delta protein
18	146.5	13.4	205	1 TVHU01	transforming prote
19	144.5	13.2	192	2 A47538	bcl-2-associated p
20	141.5	12.9	190	2 A47537	apoptosis regulato
21	132	12.1	211	2 S56873	Bak protein - huma
22	128.5	11.7	192	2 D47538	bcl-2-associated p
23	127	11.6	211	2 S56875	cdn-2 protein - hu
24	124	11.3	133	2 I53795	bcl-2-associated p
25	121	11.1	350	2 A47476	Bcl2 homolog MCL1
26	111.5	10.2	143	2 I38921	bcl-2-associated p
27	106	9.7	154	2 I58194	gene bcl-2 protein
28	93.5	8.5	172	2 I49449	hemopoietic-specif
29	93.5	8.5	115	2 A70990	cardanoyl-phosphat

30	93.5	8.5	1203	2 I55466	N-methyl-D-asparta
31	92.5	8.5	175	2 I39055	Bcl-2 related - hu
32	90.5	8.3	118	2 S70089	kor protein - hu
33	88.5	8.1	411	2 E70667	hypothetical prote
34	88	8.0	373	2 H84404	ferrichrome ABC tr
35	85.5	7.8	255	2 JC7567	Mcl-1a protein - z
36	85.5	7.8	297	2 B98172	pca operon transcr
37	85.5	7.8	600	2 D87232	conserved membrane
38	84.5	7.7	404	2 E83561	probable type II s
39	84.5	7.7	526	2 B87598	TPR domain protein
40	84.5	7.7	672	2 S46276	acetate-CoA ligase
41	84.5	7.7	1129	2 H86975	probable carbamoyl
42	84	7.7	177	2 S54778	NR-13 protein - qu
43	82.5	7.5	255	2 JC4319	uroporphyrin-III C
44	82.5	7.5	860	2 C83750	manosyltransferas
45	82	7.5	552	2 S71811	probable transcrip

#### ALIGNMENTS

##### RESULT 1

JE0203

apoptosis regulator bcl-x isoform - human

N:Alternate names: h-bcl-xbeta

C:Species: Homo sapiens (man)

C>Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 16-Jul-1999

C:Accession: JE0203

R:Ban, J.; Eckhart, L.; Weninger, W.; Milder, M.; Tschachler, E.

Biochem. Biophys. Res. Commun. 248, 147-152, 1998

A>Title: Identification of a human cDNA encoding a novel bcl-x isoform.

A:Reference number: JE0203; MUID:98340865; PMID:9675101

A:Accession: JE0203

A:Molecule type: mRNA

A:Residues: 1-227 <BAN>

A:Cross-References: GB:U72398; NID:G1622940; PIDN:AB17354.1; PID:G1622941

C:Genetics:

A:Gene: bcl-x

A:Map position: 20

C:Superfamily: bcl transforming protein

##### Query Match

Best Local Similarity 23.7%; Pred. No. 2.1e-07;

Matches 51; Conservative 29; Mismatches 78; Indels 57; Gaps 6;

QY	21	SPIDKELVAQAKRLGREYVHARLRAGLSMS-----APERA-----	56
DB	2	SQSNRELVV-----DFLSYKLSQKGYMSQFSQDVEENRTPEAPEGTESEMETPSAINGN	54
QY	57	-----SPAPGGR-----LAEVCTVLLRLGDELEQIRPSYRNVARQLHI	95
DB	55	PSWHLADSPAVNGATGHSLSLDAREVYIPMAAVQALRENGDEELATRRAFSDLTSQLHI	114
QY	96	PIQSEPVVTDALFVAGHIFPSAGITGWKVSLSYVAAGLAVDCVROAPAMVHALVDCIG	155
DB	115	---TPTAVQSEFQVYNELEFRDGVNMGRIYAFPSFGALCAVESVDKEMQVLVSRIAMMA	171
QY	156	EPVAKRLATWIRRRGGW--TDVLKCVVSTDPGGRS	188
DB	172	TYLNDHLEPWIENGSGWRTKPLVCPFSLASGORS	206

##### RESULT 2

I53744

gene bcl-2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999

C:Accession: I53744

R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.

Gene 140, 291-292, 1994

A>Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.

A:Reference number: I53744; MUID:94193015; PMID:8144041

A:Accession: I53744

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: GB:L14680; NID:9408946; PID:AAA53662.1; PID:9408947  
C:Genetics:  
A:Gene: bcl-2  
C:Superfamily: bcl transforming protein

Query Match 14.8%; Score 161.5; DB 2; Length 236;  
Best Local Similarity 23.3%; Pred. No. 2.2e-07;  
Matches 52; Conservative 34; Mismatches 80; Indels 57; Gaps 8;

28 VAQAKALG-----REYHARLLRAGLSM-----SAPERASPAAG-----61  
1 MAQAGRTGDNREIYWKYHYKLSQRYEMDGDDEDSAPLRAPTPGIRSFQESNRTPA 60  
62 -----GRLAECYVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96  
61 VHRDPAARTSPRLPIVANAGPALSPVPVHLLRRAGDDFSRRYRDRDAEMSSQLHLTP 120  
97 LOSEPVTDAFLAVAGHIFSAGITWGVSLYSVAAGLAVDCVROQAPAMVHALVDCGEE 156  
121 FTAR-----GRFATVVEELFRDGVNMGRIYAFEEFGVCMCVSVNREMSPLVDNIALMTE 176  
157 EVRKLTATLWLRRGWTDVLCV-VSTDGFRSHML-VATLCS 197  
177 YLNRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTL 219

## RESULT 3

transforming protein (bcl-2-beta) - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 24-Apr-1998  
C:Accession: B37332; S35452  
R:Aguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
A:Reference number: A37332; MUID:92375724; PMID:1508712  
A:Accession: B37332  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-216 <EGU>  
A:Cross-references: EMBL:D11381; EMBL:D11382  
C:Superfamily: bcl transforming protein

Query Match 14.4%; Score 157.5; DB 2; Length 216;  
Best Local Similarity 21.0%; Pred. No. 4.7e-07;  
Matches 45; Conservative 35; Mismatches 77; Indels 57; Gaps 6;

20 RSPDKELVAQAKALGREYHARLLRAGLSMA-----PERASPAAGGLAEVCT-----69  
7 KGYDNREIVL-----KTHYKLSQRYEMDGDDEDSAPLRAPTPAAPAAVAAAGASS 59  
70 -----VLLRLGDELEQIRPSYRNVARQLHI-P 98  
60 HHRPPGSAASVPAEGLRPAEPGVHLLRQAGDEFSRKYQRFQMSQHLHLTP 119  
99 SEPVTDAFLAVAGHIFSAGITWGVSLYSVAAGLAVDCVROQAPAMVHALVDCGEE 158  
120 AH-----GRFVAVVEELFRDGVNMGRIYAFEEFGVCMCVSVNREMSPLVDNIALMTE 175  
159 RKTATLWLRRGWTDVLCV-VSTDGFRSHMLV 192  
176 NRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTL 204

## RESULT 4

JC7383  
B-cell lymphoma 2 protein - Chinese hamster  
C:Species: Cricetus griseus (Chinese hamster)  
C>Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 08-Dec-2000  
C:Accession: JC7383

R:Tomlić, M.T.; Christmann, M.; Kaina, B.  
Biochem. Biophys. Res. Commun. 275, 899-903, 2000  
A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.  
A:Reference number: JC7383  
A:Contents: Ovary  
A:Accession: JC7383  
A:Molecule type: mRNA  
A:Residues: 1-236 <TOM>  
A:Cross-references: GB:A271720  
C:Comment: This protein has anti-apoptotic function, and supports cell survival.  
C:Genetics:  
A:Gene: bcl-2  
C:Superfamily: bcl transforming protein  
C:Keywords: B-cell lymphoma; ovary

Query Match 14.3%; Score 156.5; DB 2; Length 236;  
Best Local Similarity 22.4%; Pred. No. 6.5e-07;  
Matches 50; Conservative 36; Mismatches 80; Indels 57; Gaps 8;

28 VAQAKALG-----REYHARLLRAGLSM-----SAPERASPAAG-----61  
1 MAQAGRTGDNREIYWKYHYKLSQRYEMDGDVDAAPLGAAPTPGIRSFQESNRTPA 60  
62 -----GRLAECYVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96  
61 VHRDPAARTSPRLPIYATTPGIRSFQESNRTPA 120  
97 LOSEPVTDAFLAVAGHIFSAGITWGVSLYSVAAGLAVDCVROQAPAMVHALVDCGEE 156  
121 FTAR-----GRFATVVEELFRDGVNMGRIYAFEEFGVCMCVSVNREMSPLVDNIALMTE 176  
157 EVRKLTATLWLRRGWTDVLCV-VSTDGFRSHML-VATLCS 197  
177 YLNRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTL 219

## RESULT 5

BCL-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: 167432  
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.  
A:Reference number: 153295; MUID:95129487; PMID:7828536  
A:Accession: 167432  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: EMBL:U34964; NID:91004378; PID:AAA77687.1; PID:91004379  
C:Superfamily: bcl transforming protein

Query Match 14.3%; Score 156; DB 2; Length 236;  
Best Local Similarity 21.5%; Pred. No. 7.2e-07;  
Matches 51; Conservative 36; Mismatches 84; Indels 66; Gaps 8;

28 VAQAKALG-----REYHARLLRAGLSM-----SAPERASPAAG-----61  
1 MAQAGRTGDNREIYWKYHYKLSQRYEMDGDDEDSAPLRAPTPGIRSFQESNRTPA 60  
62 -----GRLAECYVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96  
61 VHRDPAARTSPRLPIVANAGPALSPVPVHLLRRAGDDFSRRYRDRDAEMSSQLHLTP 120  
97 LOSEPVTDAFLAVAGHIFSAGITWGVSLYSVAAGLAVDCVROQAPAMVHALVDCGEE 156  
121 FTAR-----GRFATVVEELFRDGVNMGRIYAFEEFGVCMCVSVNREMSPLVDNIALMTE 176  
157 EVRKLTATLWLRRGWTDVLCV-VSTDGFRSHM-----LVATLCSFGRL 202  
177 YLNRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTLALVGCITLGLAYL 233







QY 57 -----SPAGGR-----LAECVTLRLGDELEQIRPSYRNVAROLHI 95  
 DB 55 PSMHLADSPAVNGATGSHSSLDAREVLPMAAVQAOLREAGDELELRRRFSOLTSOLHI 114  
 QY 96 PLOSEPVTDAFLAVAGHIFSGITGKVVSLYSVAAGLAVDCVROAQPAMVHALVCLIG 155  
 DB 115 ---TPGTAVQSFQVYNVELFRDGVNMGRIYAFSSFGALCVESVDKEMQVLVSRIASMA 171  
 QY 156 EFVRKTLATVLRRCGW 172  
 DB 172 TYLNDHLEPWIQENGW 188  
 RESULT 13  
 B47537  
 apoptosis regulator bcl-xl - human  
 N:Alternate names: bcl-2-related protein  
 N:Contains: apoptosis regulator bcl-xs  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Jul-1999  
 C:Accession: B47537, C47537  
 R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
 Cell 74, 597-608, 1993  
 A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic  
 A:Reference number: A47537; MUID:93364977; PMID:8358789  
 A:Accession: B47537  
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <BOI>  
 A:Cross-references: GB:L20121; NID:9510900; PIDN:CAAB0661.1; PID:9510901  
 A:Accession: C47537  
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-69, 'G', 71-125, 189-233 <BO2>  
 A:Cross-references: GB:L20122; NID:9623236; PIDN:CAAB0662.1; PID:9623237  
 C:Genetics:  
 A:Gene: GDB:BCL2L  
 A:Cross-references: GDB:228079  
 C:Superfamily: bcl transforming protein  
 C:Keywords: alternative splicing; apoptosis  
 F1-233/Product: apoptosis regulator bcl-xl #status predicted <MA2>  
 F1-135,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>  
 Query Match 13.8%; Score 150.5; DB 2; Length 233;  
 Best Local Similarity 22.3%; Pred. No. 2.3e-06;  
 Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;  
 QY 21 SPDKELVQAOKALGREYVARLLRAGLSMS-----APERA----- 56  
 DB 2 SOSNRELVV-----DLSYKLSQKGYSSQPSDVEENFTPEAEGTESMETPSALINGN 54  
 QY 57 -----SPAGGR-----LAECVTLRLGDELEQIRPSYRNVAROLHI 95  
 DB 55 PSMHLADSPAVNGATGSHSSLDAREVLPMAAVQAOLREAGDELELRRRFSOLTSOLHI 114  
 QY 96 PLOSEPVTDAFLAVAGHIFSGITGKVVSLYSVAAGLAVDCVROAQPAMVHALVCLIG 155  
 DB 115 ---TPGTAVQSFQVYNVELFRDGVNMGRIYAFSSFGALCVESVDKEMQVLVSRIASMA 171  
 QY 156 EFVRKTLATVLRRCGW 172  
 DB 172 TYLNDHLEPWIQENGW 188  
 RESULT 14  
 TRANSFORMAL  
 transforming protein bcl-2, splice form alpha - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999  
 C:Accession: C37332; A29409; S02452; A24428; A27622; B27622  
 R:Tsujimoto, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie

A:Reference number: A37332; MUID:92375724; PMID:1508712  
 A:Accession: C37332  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-239 <EGU>  
 A:Note: this report is a correction  
 R:Tsujimoto, Y.; Croce, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986  
 A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the g  
 A:Reference number: A29409; MUID:86259760; PMID:3523487  
 A:Accession: A29409  
 A:Molecule type: mRNA  
 A:Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>  
 A:Cross-references: GB:M13994; NID:9179366; PIDN:AAA51813.1; PID:9179367  
 A:Note: this sequence has been corrected in reference A37332  
 R:Sefto, M.; Jaeger, U.; Hockett, R.D.; Granger, W.; Bennett, S.; Goldman, P.; Korsm  
 EMBO J. 7, 123-131, 1988  
 A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bc  
 A:Reference number: S02452; MUID:88196071; PMID:2834197  
 A:Accession: S02452  
 A:Molecule type: mRNA  
 A:Residues: 1-239 <SEM>  
 R:Cleary, M.L.; Smith, S.D.; Sklar, J.  
 Cell 47, 19-28, 1986  
 A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin  
 A:Reference number: A24428; MUID:87002488; PMID:2875799  
 A:Accession: A24428  
 A:Molecule type: mRNA  
 A:Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>  
 A:Cross-references: GB:M14745; NID:9179370; PIDN:AAA55591.1; PID:9179371  
 R:Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A  
 Oncogene Res. 2, 263-275, 1988  
 A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma  
 A:Reference number: A27622; MUID:88217344; PMID:3285301  
 A:Accession: A27622  
 A:Molecule type: mRNA  
 A:Residues: 1-58, 'T', 60-239 <HUA>  
 A:Accession: B27622  
 A:Molecule type: DNA  
 A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA>  
 A:Note: the sequence was determined from the germine gene  
 C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocati  
 C:Genetics:  
 A:Gene: GDB:BCL2  
 A:Cross-references: GDB:119031; OMIM:151430  
 A:Map position: 18q21.3-18q21.3  
 C:Function:  
 A:Description: blocks apoptosis in hematopoietic cells  
 C:Superfamily: bcl transforming protein  
 C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr  
 Query Match 13.8%; Score 150.5; DB 1; Length 239;  
 Best Local Similarity 21.9%; Pred. No. 2.3e-06;  
 Matches 46; Conservative 36; Mismatches 75; Indels 53; Gaps 7;  
 QY 37 EYVHARILRAGLSM-----SADERSPADG-----GRLAECT-- 69  
 DB 17 KYIHVYKLSQGYEMDAGDVGAAPGAPADIGFSQPGHTRHPAASRDPAVARTSPLOTTPA 76  
 QY 70 -----VLRLGDELEQIRPSYRNVAROLHI--PLOSEPVTDAFLA 109  
 DB 77 APGAAGPALSPPVPPVHLLTQAGDDFSRRYRDRFEMSSOLHLPFTLR---GREAT 132  
 QY 110 VAGHIFSGITGKVVSLYSVAAGLAVDCVROAQPAMVHALVCLIGEFVRKTLATVLR 169  
 DB 133 VEFELFRDGVNMGRIYAFSSFGALCVESYVRENSPLVDNIALMNTGYLRLHATWICDN 192  
 QY 170 GGTVDLVLCV-VSTDPGFSRHWL-VATLCS 197  
 DB 193 GMDAFVELGSPWRPLFDSWLSLTKTLLS 222  
 RESULT 15

bcl-2-associated protein x, beta splice form - human  
N:Alternate names: Bax; programmed cell death membrane protein x beta  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 17-Nov-2000  
C:Accession: BA7538  
R:Olteanu, Z.N.; Milliman, C.L.; Korsmeyer, S.J.  
Cell 74, 609-619, 1993  
A>Title: Bcl-2 heterodimerizes in vivo with a conserved homology, Bax, that accelerates F

A:Reference number: A47538; MUID:93364978; PMID:8358790  
A:Accession: BA7538  
M:Molecule type: mRNA  
A:Residues: 1-218 <Full>  
A:Cross-references: GB:T22474; NID:g388167; PIDN:AAA03620.1; PID:g388168  
A>Note: The amino end of the mature protein is blocked  
C:Genetics:  
A:Gene: GDB:BAX  
A:Cross-references: GDB:228082; OMIM:600040  
A:Map position: 19q13.3-19q13.4  
C:Superfamily: bcl transforming protein  
C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match            13.7%; Score 149..5; DB 2; Length 218;  
Best Local Similarity     28.8%; Pred. No. 2,6e-06;  
Matches    46; Conservative       29; Mismatches      72; Indels          13; Gaps            6;

OY            22 PDKKLVAQAKALGHE-YVHARLLRAGLSWSAPERA-SPA-PGGRLAEVCYLRLGDEL 78  
             | :  
DB            13 PISSSQIKMTGALLQGFIODRAGRMC--GEAPELADLPVPODASTKSLSECKRIQDEL 70  
  
OY            79 EDIRSVYNRVNAQRQLHIPILOSEPVVTDAFLAVAGIHFSAG-IITMGKVSLTYSVAAGLAVD 137  
             :  
DB            71 DS-----NMELQMIAIVADPTDSPREVEFFRYAADMFSDGNPFNNCRVALATLYFPASKVLTK 123  
  
OY            138 CVRAQAQPAMVAIYDCLEFVRKTILATLWLRRGCTDYLK 177  
  
DB            124 ALCTRVPPLIRTMGWTLDFLTRERLGMIODOGCVNRWLK 163

Search completed: April 29, 2003, 11:26:33  
Job time : 14.3473 secs

GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:16:46 ; Search time 32.539 Seconds  
(without alignments)  
872.393 Million cell updates/sec

Title: US-09-682-667-2  
Perfect score: 1094  
Sequence: 1 MEVLRRSSVFPAEIMDAEDR.....TLCSPGRFLKAAFFILPER 213

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq\_101002.\*  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1094	100.0	213	20	AAV14153
2	1076	98.4	213	20	AAV14155
3	1052	96.2	213	21	AAAB41444
4	839.5	76.7	170	20	AAV14154
5	828.5	75.7	170	20	AAV14156
6	727	66.5	176	21	AAAB58949
7	671	61.3	134	22	AAAB56655
8	244.5	22.3	846	22	AAAB64401
9	234	21.4	247	22	AAAB63760
10	159	14.5	235	19	AAW48312

11	158	14.4	485	22	AAU00222
12	156.5	14.3	239	22	AAAB48288
13	156.5	14.3	239	22	AAAB50537
14	155.5	14.2	233	22	AAAB73304
15	155	14.2	232	17	AAW01020
16	155	14.2	232	20	AAW94347
17	154.5	14.1	233	22	AAAB73303
18	154.5	14.1	236	20	AAW87811
19	154.5	14.1	236	22	AAAB74128
20	154.5	14.1	236	22	AAAB35131
21	154.5	14.1	236	22	AAU76554
22	154.5	14.1	239	22	AAAG64037
23	152.5	13.9	221	18	AAW10688
24	152.5	13.9	239	17	AAW02383
25	152.5	13.9	239	22	AAAG64036
26	152.5	13.9	239	22	AAAG64038
27	152	13.9	239	21	AAV69203
28	151.5	13.8	239	9	AAAB0987
29	151.5	13.8	239	14	AAAR42312
30	151.5	13.8	239	16	AAAR70331
31	151.5	13.8	239	16	AAAR71404
32	151.5	13.8	239	17	AAW01018
33	151.5	13.8	239	19	AAW40217
34	151.5	13.8	239	20	AAW94345
35	151.5	13.8	239	20	AAW87812
36	151.5	13.8	239	22	AAE08573
37	151.5	13.8	239	22	AAAG64035
38	151.5	13.8	239	22	AAAB74129
39	151.5	13.8	239	23	AAAB75986
40	151.5	13.8	239	23	AAAB05227
41	151.5	13.8	272	19	AAV21120
42	150.5	13.8	233	16	AAAB68887
43	150.5	13.8	233	17	AAW05821
44	150.5	13.8	233	18	AAW31530
45	150.5	13.8	233	21	AAV83223

#### ALIGNMENTS

RESULT 1	AAV14153	standard; Protein: 213 AA.
ID	AAV14153	
XX	AAV14153:	
AC	AAV14153:	
XX		
DT	27-JUL-1999	(first entry)
XX		
DE	Rat Bok protein sequence.	
XX		
KW	Bok protein; Bcl-2-related ovarian killer; BH31 variant; endometriosis;	
KW	pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;	
KW	reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;	
KW	ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;	
XX		
OS	Rattus rattus.	
XX		
PN	W09924453-A1.	
PD	20-MAY-1999.	
XX		
PF	04-NOV-1998;	98WO-US23523.
XX		
PR	07-NOV-1997;	97US-0064943.
XX		
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.	
XX		
PI	Hsu SY, Hsueh AJW;	
XX		
DR	WPI: 1999-327356/27.	
XX	N-PSDB: AAX61103.	
XX		

LEF-Bcl-XL apoptos  
Human Bcl-2 protei  
Human Bcl-2 protei  
Mutant rat Bcl-XL  
Apoptosis-blocking  
Human Bcl-2 mutant  
Rat wild-type Bcl-  
A murine Bcl-2 pro  
Murine bcl-2. Mus  
Murine Bcl-2. Mus  
Murine Bcl-2 polyP  
Human Bcl-2 protei  
Bax omega protein,  
Human Bcl2. Homo  
Human Bcl-2 protei  
Human Bcl-2 protei  
Amino acid sequenc  
Sequence of bcl-2-  
Bcl-2 oncogene pro  
Human bcl-2 protei  
Human bcl-2 alpha  
Apoptosis-blocking  
Human bcl-2. Homo  
Human Bcl-2 wild-t  
A human Bcl-2-alph  
Human Bcl-2 protei  
Human Bcl-2 protei  
Human bcl-2alpha.  
Protein sequence.  
Human D34A caspase  
Human bcl2 proto-o  
Human thymus BCL-X  
Bcl-XL protein. H  
Human anti-apoptot  
Bcl-x polypeptide.

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 PS Claim 2; Page 53-54; 62pp; English.  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 SQ Sequence 213 AA;  
 Query Match 100.0%; Score 1094; DB 20; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-111;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 QY 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDAPFLAVAGHIFSAGIT 120  
 DB 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDAPFLAVAGHIFSAGIT 120  
 QY 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEFVRKLTATWLRRGGMTDVLKCV 180  
 DB 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEFVRKLTATWLRRGGMTDVLKCV 180  
 QY 181 STDGFRSHMLVATLCSPGRFLKAAFLLLP 213  
 DB 181 STDGFRSHMLVATLCSPGRFLKAAFLLLP 213  
 RESULT 2  
 ID AAY14155 standard; Protein: 213 AA.  
 AC AAY14155;  
 XX 27-JUL-1999 (first entry)  
 DE Human Bok protein sequence.  
 KW Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; human.  
 XX Homo sapiens.  
 OS  
 PN WC0924453-A1.  
 XX  
 PD 20-MAY-1999.  
 XX  
 PF 04-NOV-1998; 98WC-US23523.  
 XX  
 PR 07-NOV-1997; 97US-0064943.  
 XX

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Hsu SY, Hsueh AJW;  
 XX  
 DR WPI: 1999-327356/27.  
 DR N-PSDB: AAX61105.  
 XX  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 PS Claim 2; Page 55-56; 62pp; English.  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 SQ Sequence 213 AA;  
 Query Match 98.4%; Score 1076; DB 20; Length 213;  
 Best Local Similarity 98.6%; Pred. No. 3.3e-109;  
 Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 QY 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDAPFLAVAGHIFSAGIT 120  
 DB 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDAPFLAVAGHIFSAGIT 120  
 QY 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEFVRKLTATWLRRGGMTDVLKCV 180  
 DB 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEFVRKLTATWLRRGGMTDVLKCV 180  
 QY 181 STDGFRSHMLVATLCSPGRFLKAAFLLLP 213  
 DB 181 STDGFRSHMLVATLCSPGRFLKAAFLLLP 213  
 RESULT 3  
 ID AAB41444 standard; Protein: 213 AA.  
 AC AAB41444;  
 XX 08-FEB-2001 (first entry)  
 DE Human ORFX ORF1208 polypeptide sequence SEQ ID NO:2416.  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnerability; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antihemetic; antithyroid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

KM cholesterol ester storage; systemic lupus erythematosus; infection;  
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KM thrombosis; contraceptive.  
 XX Homo sapiens.  
 OS  
 XX  
 PN MO200058473-A2.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 31-MAR-2000; 2000MO-US08621.  
 XX  
 PR 31-MAR-1999; 99US-0127607.  
 PR 02-APR-1999; 99US-0127636.  
 PR 05-APR-1999; 99US-0127728.  
 PR 30-MAR-2000; 2000US-0540763.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinketsu RA, Leach M;  
 XX  
 DR WPI: 2000-602362/57.  
 DR N-PSDB: AAC75653.  
 XX  
 PT Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 XX  
 PS Claim 11: Page 1750-1751; 5507pp; English.  
 XX  
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytoskeletal; hepatotropic; vulnerrary;  
 CC antiproliferative; antiparkinsonian; neurotropic; immunosuppressive;  
 CC osteoparic; anticonvulsant; antiarthritic; immunosuppressive;  
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antipneumatic;  
 CC antihypertoid; and antianemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 CC  
 XX  
 SQ Sequence 213 AA;  
 Query Match 96.2%; Score 1052; DB 21; Length 213;  
 Best Local Similarity 96.2%; Pred. No. 1.4e-106;  
 Matches 205; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MEVLRRSSVFAAEIMDAFDRSPDKELVAQAKALGREYVARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPDKELVAQAKALGREYVARLLRAGLSMSAPERASAP 60  
 QY 61 GGRLAEVCYLLRLGDELEDIRSVYRNVAROLHIPILOSEPVVTDFAVLAAGHIFSAGIT 120  
 DB 61 GGRLAEVCYLLRLGDELEDIRSVYRNVAROLHIPILOSEPVVTDFAVLAAGHIFSAGIT 120  
 QY 121 MGRVSVLSYVAAGLAADVCAQAPAMVHALVYDCLGEFVRATLAWLRRCGMDVLKCV 180  
 DB 121 MGRVSVLSYVAAGLAADVCAQAPAMVHALVYDCLGEFVRATLAWLRRCGMDVLKCV 180  
 QY 181 STDPGFRSHWLVAALCSGFRFLKAAPFLPPER 213

DB 181 STDPGFRSHWLVAALCSGFRFLKAAPFLPPER 213  
 RESULT 4  
 ID AAY14154  
 AC AAY14154 standard; Protein; 170 AA.  
 XX  
 AC AAY14154;  
 XX  
 DT 27-JUL-1999 (first entry)  
 XX  
 DE Rat Bok protein sequence.  
 XX  
 KW Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; rat.  
 XX  
 OS Rattus rattus.  
 XX  
 PN WO924453-A1.  
 XX  
 PD 20-MAY-1999.  
 XX  
 PF 04-NOV-1998; 98MO-US23523.  
 XX  
 PR 07-NOV-1997; 97US-0064943.  
 XX  
 PA (STRD ) UNIV IELAND STANFORD JUNIOR.  
 XX  
 PI Hsu SY, Hsueh AJW;  
 XX  
 DR WPI: 1999-327356/27.  
 DR N-PSDB: AAX61104.  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 XX  
 PS Claim 2: Page 54-55; 62pp; English.  
 XX  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 XX  
 SQ Sequence 170 AA;  
 Query Match 76.7%; Score 839.5; DB 20; Length 170;  
 Best Local Similarity 79.3%; Pred. No. 1.7e-83;  
 Matches 169; Conservative 0; Mismatches 1; Indels 43; Gaps 1;  
 QY 1 MEVLRRSSVFAAEIMDAFDRSPDKELVAQAKALGREYVARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPDKELVAQAKALGREYVARLLRAGLSMSAPERASAP 60  
 QY 61 GGRLAEVCYLLRLGDELEDIRSVYRNVAROLHIPILOSEPVVTDFAVLAAGHIFSAGIT 120  
 DB 61 GGRLAEVCYLLRLGDELEDIRSVYRNVAROLHIPILOSEPVVTDFAVLAAGHIFSAGIT 120

Db 61 GGRLAECVTLLRL-----GIT 77

Qy 121 WCKVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
|||||  
Db 78 WCKVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 137  
|||||

Qy 181 STDGFRSHMLVATLCSFGRLKAAFFLLPER 213  
|||||  
Db 138 STDGFRSHMLVATLCSFGRLKAAFFLLPER 170  
|||||

RESULT 5  
AAV14156  
ID AAV14156 standard; Protein; 170 AA.  
XX  
AC AAV14156;  
XX  
DT 27-JUL-1999 (first entry)  
XX  
DE Human Bok protein sequence.  
XX  
KW Bok protein; Bcl-2-related ovarian killer; BH31 variant; endometriosis;  
KM pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KM reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KM ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
KM proliferative disorder; human.  
XX  
OS Homo sapiens.  
XX  
PN WO924453-A1.  
XX  
PD 20-MAY-1999.  
XX  
PF 04-NOV-1998; 98WO-US23523.  
XX  
PR 07-NOV-1997; 97US-0064943.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
PI Hsu SY, Hsueh AW;  
XX  
DR WPI; 1999-327356/27.  
XX  
DR N-PSDB; AAX61106.  
XX  
PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
PR protein and its related gene  
XX  
PS Claim 2; Page 57-58; 62pp; English.  
XX  
CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH31 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.  
XX  
SQ Sequence 170 AA;

Query Match 75.7%; Score 828.5; DB 20; Length 170;  
Best Local Similarity 78.4%; Pred. No. 2.7e-82;  
Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

Qy 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLRAGLSWSPERASPAP 60  
|||||  
Db 1 MEVLRRSSVFAAEIMDAFDRWPTDKELVAQAKALGREYHARLRAGLSWSPERASPAP 60  
|||||

Qy 61 GGRLAECVTLLRLDGELEQIRPSYRNARQLHTLPQSEPVYTDALFVAQHTSAGIT 120  
|||||  
Db 61 GGRLAECVTLLRL-----GIT 77  
|||||

Qy 121 WCKVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 180  
|||||  
Db 78 WCKVSVLSVAAGLAVDCVROQAPAMVHALVDCLEGFVAKRTLATWLRRGWTDVLCVY 137  
|||||

Qy 181 STDGFRSHMLVATLCSFGRLKAAFFLLPER 213  
|||||  
Db 138 STDGFRSHMLVATLCSFGRLKAAFFLLPER 170  
|||||

RESULT 6  
AAB58949  
ID AAB58949 standard; Protein; 176 AA.  
XX  
AC AAB58949;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.  
XX  
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
KM neotropic; neuroprotective; antiviral; anti-allergic; hepatotropic;  
KM antidiabetic; anti-inflammatory; antilucer; vulnerary; anticonvulsant;  
KM antibacterial; antifungal; antiparasitic; cardiant; immune disorder;  
KM Addison's disease; allergy; autoimmune hemolytic anaemia;  
KM autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
KM cardiovascular disorder; wound healing; neurological disease.  
XX  
OS Homo sapiens.  
XX  
PN WO20005173-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US05881.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2000-611515/58.  
XX  
DR N-PSDB; AAF21852.  
XX  
PT New human breast and ovarian cancer associated gene sequences and the  
PR polypeptides encoded by these genes, useful in the prevention,  
PT treatment and diagnosis of cancer, immune disorders, cardiovascular  
PT disorders and neurological diseases -  
XX  
PS Claim 11; Page 1103; 1299pp; English.  
XX  
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
CC associated with breast and ovarian cancer. Included in the invention are  
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
CC isolation and characterisation of the DNA and protein sequences of the  
CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
CC neotropic; neuroprotective; antiviral; anti-allergic; hepatotropic;  
CC antidiabetic; anti-inflammatory; antilucer; vulnerary; anticonvulsant;  
CC antibacterial; antifungal; antiparasitic and cardiant activity. The  
CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
CC particularly breast and ovarian cancer. The nucleic acid sequences,







PT develop products for treating autoimmune disorders or  
PT immunodeficiencies

PS Claim 8; Page 84; 123pp; English.

XX This amino acid sequence comprises mouse BCL-x gamma, a novel,  
CC isoform of the BCL-x family that has a novel C-terminal gamma  
CC domain. The sequence was deduced from an isolated cDNA clone  
CC (see AAV17638) from a thymus cDNA library. n ankyrin domain and which  
CC is predominantly expressed in T-lymphocytes and which is associated  
CC with resistance to apoptosis. BCL-x gamma polypeptides can be  
CC expressed in host cells and used to screen for modulator compounds.  
CC BCL-x gamma activity can be down-modulated in order to ameliorate  
CC an autoimmune disorder such as graft-versus-host disease, cases of  
CC transplantation, and autoimmune diseases e.g. diabetes mellitus,  
CC arthritis, multiple sclerosis, myasthenia gravis, systemic lupus  
CC erythematosus, autoimmune thyroiditis, dermatitis, psoriasis,  
CC Sjogren's syndrome, alopecia areata, aphthous ulcer, lrlitis,  
CC arthropod bite, Crohn's disease, ulcerative colitis, asthma,  
CC conjunctivitis, keratoconjunctivitis, vaginitis, proctitis,  
CC cutaneous lupus erythematosus, scleroderma, vaginitis, proctitis,  
CC drug eruptions, leprosy reversal reactions, erythema nodosum leprosum,  
CC autoimmune uveitis, allergic encephalomyelitis, acute necrotizing  
CC haemorrhagic encephalopathy, idiopathic bilateral progressive  
CC sensorineural hearing loss, aplastic anaemia, pure red cell anaemia,  
CC idiopathic thrombocytopenia, polyorchiditis, Wegener's granulomatosis,  
CC chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue,  
CC lichen planus, Graves ophthalmopathy, sarcoidosis, primary biliary  
CC cirrhosis, uveitis posterior, and interstitial lung fibrosis.  
CC BCL-x gamma activity can be upmodulated, e.g. by gene therapy, to  
CC ameliorate e.g. severe combined immunodeficiency, adenosine deaminase  
CC deficiency, purine nucleoside phosphorylase deficiency, MHC class II  
CC deficiency, reticular dysgenesis, X-linked agammaglobulinemia,  
CC X-linked hypogammaglobulinemia, Ig deficiency with increased IGM,  
CC Ig heavy chain-gene deletions, k-chain deficiency Iga deficiency,  
CC selective deficiency of IgG subclass, common variable  
CC immunodeficiency, transient hypogammaglobulinemia of infancy,  
CC Wiskott-Aldrich syndrome, ataxia telangiectasia, DiGeorge syndrome,  
CC Bloom syndrome, Fanconi anaemia, and Down syndrome-related  
CC immunodeficiency, as well as other syndromes associated with  
CC immunodeficiency and immunodeficiencies resulting from other causes,  
CC such as HIV disease and AIDS. Additionally, it may be desirable to  
CC upregulate BCL-x gamma activity to increase T cell survival in the  
CC case of other disorders, e.g. cellular responses to tumours, or  
CC pathogens.

XX Sequence 235 AA;

Query Match 14.5%; Score 159; DB 19; Length 235;  
Best Local Similarity 22.3%; Pred. No. 5, 2e-09;  
Matches 52; Conservative 31; Mismatches 80; Indels 70; Gaps 8;

OY 21 SPDKELVQAKALGREYHARLRAGLSMS-----APEKA----- 56  
DB 2 SOSNRELVV-----DFLSYKLSQKGYMSQPSDVENKTEPEETEARPPSAINGN 54  
OY 57 -----SPAPGR-----LAECVTLLRLGDELEQIRPSYRVAROLHI 95  
DB 55 PSMHLADSPAVNCAHSSSLDAREYIPMAAYQALREANGDEFLATRRFSLTQSLHI 114  
OY 96 PLOSEPVYDAFLAVAGHIFPSAGITGKVVSLYSVAGLAIVDCVROAQPAMVHALVCLG 155  
DB 115 ---TPGTAVQSFQVYVNELEFRDGVNMGRIYAFPSFGALCVESVDKEMQVLSRIASWMA 171  
OY 156 EPYRKRLAMLRKRGW-----TDVLKCVYSTDPGRFSH-----WLYAT 194  
DB 172 TYLNDHLEPDIENGWGVSGGTPLRSVPRRLVQV--PGVAEHVCDPSLWEVET 223

RESULT 11  
AAU00222  
ID AAU00222 standard; Protein; 485 AA.  
XX

AC AAU00222;  
XX 31-MAY-2001 (first entry)

DE LFn-Bcl-XL apoptosis-modifying fusion protein.

XX Human; LFn-Bcl-XL; apoptosis; cancer; spinal muscular atrophy;  
KW Anthrax lethal factor; neoplasm; tumour; hyper-proliferation;  
KW Alzheimer's disease; neurodegenerative disorder; stroke;  
KW transient ischemic neuronal injury; spinal cord injury;  
KW Huntington's disease.

OS Chimeric - Homo sapiens.

OS Chimeric - Corynebacterium diptheriae.

OS Chimeric - Synthetic.

FT Key Location/Qualifiers

FT Region 5..10

FT Region /note="6x histidine tag"

FT Region /note="Anthrax lethal factor amino acids 1 to 255"

FT Region /note="Bcl-XL amino acids 1 to 209"

XX WO200112661-A2.

XX 22-FEB-2001.

XX 15-AUG-2000; 2000MO-US22293.

XX 16-AUG-1999; 99US-0149220.

XX (HARD ) HARVARD COLLEGE.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Youle RJ, Liu X, COLLIER RJ;

XX WPI: 2001-218343/22.

XX N-PSDB; AAS00250.

PT Novel fusion protein for modifying apoptosis in target cell and  
PT reducing apoptosis after transient ischemic neuronal injury, has two  
PT domains which target protein to a cell and modifies apoptotic response  
PT of cell

PS Claim 4; Page 64-65; 65pp; English.

XX The sequence represents the amino acid sequence of LFn-Bcl-XL apoptosis-  
CC modifying fusion protein comprising anthrax lethal factor (LF) sequence  
CC fused to Bcl-XL. The functional apoptosis-modifying fusion protein is  
CC capable of binding a target cell and integrating into or crossing a  
CC cellular membrane of the target cell. The apoptosis-modifying fusion  
CC protein comprises at least two domains: the DFR domain, which targets  
CC the fusion protein to the target cell and the Bcl-XL domain, which  
CC modifies an apoptotic response of the target cell. The fusion protein is  
CC useful for modifying (inhibiting or enhancing) apoptosis in a target  
CC cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage,  
CC epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It  
CC is also useful for reducing apoptosis in a subject after transient  
CC ischemic neuronal injury, especially spinal cord injury. The fusion  
CC protein may be used to treat various diseases and injury conditions  
CC through inhibition or enhancement of apoptotic cellular response,  
CC including neurodegenerative disorders such as Alzheimer's disease,  
CC Huntington's disease, spinal muscular atrophy, stroke episodes and  
CC unregulated cell growth as in tumours and various cancers. The apoptosis-  
CC modifying fusion protein can be delivered effectively throughout the body  
CC and targeted to selective tissue and cells.

XX Sequence 485 AA;

Query Match 14.4%; Score 158; DB 22; Length 485;  
Best Local Similarity 21.8%; Pred. No. 1, 7e-08;  
Matches 47; Conservative 33; Mismatches 88; Indels 48; Gaps 4;

QY 2 EYLRRSSVFAEIMDAFDRSPDKELVAQAKALGREYVHARLLRAGLSWS----- 51  
 Db 252 DVLQIYAEAFAYMKFNQEOEINLSMSOSNRELVDFLSYKLSQKGYSWSGFSDVEENRT 311  
 QY 52 -APEKA-----SPAPGR-----LABEYCTVLLRLCD 76  
 Db 312 EAPBGTSEBEMETPSAINGNPNWHLADSPAVNGATJAHSSSLDAREVIYPMAAVQALREAGD 371  
 QY 77 ELEQIRPSYRYNVARQLHPIQSEPVYTDAPLAVAGHIFPSAGITWKGKVSLSVAAGLAV 136  
 Db 372 EPELRYRRAFSLTSLQHLT---TPGTAVOSFEQVYNELFRDGVNNGRIYAFESFGALCV 428  
 QY 137 DCVROAQPAMVHALYDCIGEFYRKTLATWLRRCGM 172  
 Db 429 ESDVDEMOVLVSRIAAMATYLDHLEPWIOENGGM 464

## RESULT 12

AAB48288  
 ID AAB48288 standard; protein: 239 AA.

AC AAB48288;

DT 02-APR-2001 (first entry)

DE Human BCL-2 protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
 KM CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytostatic.

XX Homo sapiens.

XX WO200075184-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15449.

XX 04-JUN-1999; 99US-0137494.

XX (UYYA ) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.

XX N-PSDB; AAC84600.

PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins -

PS Claim 5; Page 104-108; 162pp; English.

CC The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
 CC cullin/CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours.

CC Sequence 239 AA;

Query Match 14.3%; Score 156.5; DB 22; Length 239;

Best Local Similarity 22.4%; Pred. No. 1e-08;

Matches 47; Conservative 36; Mismatches 74; Indels 53; Gaps 7;

QY 37 EYVHARLLRAGLSW-----SAPERASAPG-----GRLAEVCT-- 69  
 Db 37 EYVHARLLRAGLSW-----SAPERASAPG-----GRLAEVCT-- 69

Db 17 KIYHKLSQRYEWDAGVGAAPGAAPAGIFSSQPGHTPTTAASRDPAVTSPLQTPA 76  
 QY 70 -----VLLRLGDELEQIRPSYRYNVARQLH-PIQSEPVYTDAPLA 109  
 Db 77 APGAAGAPALSPVPVYVHLLTLRQAGDDPSRRYRROFAEWSROLHLPTTAR-----GRFAT 132  
 QY 110 VAGHIFPSAGITWKGKVSLSVAAGLAVDCVROAQPAMVHALYDCIGEFYRKTLATWLRRR 169  
 Db 133 VVEELFRDGVNNGRIYAFEFEGVCMCVESVNRMSPLDNIALMMTEYLNRHLHTWIDN 192  
 QY 170 GGWTDVLCV-VSTDGFRSHML-VATLCS 197  
 Db 193 GGMDFAVELYGPSMRPLFDEFSWLSTKLTL 222

## RESULT 13

AAB50537  
 ID AAB50537 standard; Protein: 239 AA.

AC AAB50537;

DT 16-MAR-2001 (first entry)

DE Human BCL-2 protein sequence SEQ ID NO:2.

XX Human; Bcl-2; Bcl-xL; Bax; VDAC; apoptosis inhibitor; detection;  
 KM apoptosis promoter; diagnosis.

XX Homo sapiens.

XX JP2000287689-A.

XX 17-OCT-2000.

XX 08-APR-1999; 99JP-0101888.

XX 08-APR-1999; 99JP-0101888.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2001-065575/08.

XX N-PSDB; AAC90809.

PT Screening of an apoptosis inhibitor or promoter which can be used as a  
 PT drug and a diagnostic agent for various diseases caused by apoptosis  
 PT inhibition or apoptosis promotion -

PS Claim 11; Page 13-14; 22pp; Japanese.

CC The present invention describes a method for screening for an apoptosis  
 CC inhibitor or an apoptosis promoter in which VDAC-1 liposome, an index  
 CC substance which can pass VDAC and a sample are incubated and the change  
 CC in the concentration of the index substance during the incubation is  
 CC detected to judge the presence of apoptosis inhibition or apoptosis  
 CC promotion. The apoptosis inhibitor or the apoptosis promoter can be  
 CC used as a drug and a diagnostic agent for various diseases caused by  
 CC apoptosis inhibition or apoptosis promotion. The present sequence  
 CC represents the human Bcl-2 protein, which is an apoptosis inhibitor  
 CC used in the exemplification of the present invention.

CC Sequence 239 AA;

Query Match 14.3%; Score 156.5; DB 22; Length 239;

Best Local Similarity 22.4%; Pred. No. 1e-08;

Matches 47; Conservative 36; Mismatches 74; Indels 53; Gaps 7;

QY 37 EYVHARLLRAGLSW-----SAPERASAPG-----GRLAEVCT-- 69  
 Db 17 KIYHKLSQRYEWDAGVGAAPGAAPAGIFSSQPGHTPTTAASRDPAVTSPLQTPA 76  
 QY 70 -----VLLRLGDELEQIRPSYRYNVARQLH-PIQSEPVYTDAPLA 109  
 Db 77 APGAAGAPALSPVPVYVHLLTLRQAGDDPSRRYRROFAEWSROLHLPTTAR-----GRFAT 132

OY 110 VAGHIFSGITMGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGFEVFKTLATWLRRR 169  
 DB 133 VVEELFRDGVNMGRIYAFEFPGVCMCVESVNRMSPLVINIALMPEYLRHRLHTWIOQN 192  
 OY 170 GGWTDVLCV-VSTDPGFRSHWL-VATLCS 197  
 DB 193 GGDVAFVELYGPSMRPLDFPSWLTSLTKLTS 222

## RESULT 14

AAB73304 ID AAB73304 standard; Protein; 233 AA.

AC AAB73304;

DT 22-MAY-2001 (first entry)

DE Mutant rat Bcl-xL protein, Bcl-xFNK.

KM Rat Bcl-xL mutant; Bcl-xFNK; apoptosis inhibitor; membrane permeable;

KW programmed cell death inhibitor; wild-type; antiapoptotic; cell death

OS Rattus norvegicus.

OS Synthetic.

PN WO200112807-A1.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-JP05502.

PR 17-AUG-1999; 99JP-0230642.

PA (NISC-) JAPAN SCT & TECHNOLOGY CORP.

PI Ohta S, Asoh S;

DR WPI: 2001-211219/21.

PT Modified cDNA of rat bcl-x gene and encoded protein with membrane permeability to enhance uptake for effective inhibition of cell death e.g. apoptosis, useful in remedies for diseases associated with cell death.

PS Claim 1; Page 46-47; 56pp; Japanese.

CC The invention relates to a mutant rat Bcl-x protein and the cDNA

CC encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the

CC substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL

CC protein. The invention also encompasses recombinant vectors and host

CC cells comprising the modified nucleic acid sequence. The mutant Bcl-x

CC protein is able to permeate the cell membrane, thus enhancing its

CC ability to be taken up into a cell and to act as an inhibitor of

CC apoptosis (programmed cell death). Bcl-xFNK and nucleic acids encoding

CC it are useful in remedies for diseases associated with cell death and

CC in additives for maintaining the stability of transplanted cells and

CC organs. The present sequence represents the mutant rat Bcl-xL protein,

CC Bcl-xFNK.

XX Bcl-xFNK.

XX Sequence 233 AA;

XX Query Match 14.2%; Score 155.5; DB 22; Length 233;

XX Best Local Similarity 22.3%; Pred. No. 1.2e-08; Indels 55; Gaps 5;

XX Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;

OY 21 SPTDKELVQAOKALGREYVHARLRAGLSWS-----APERA----- 56

DB 2 SQGNRELIV-----DFLSYKLSQKGFSSNSDVENTEAPDEPEPEPERSAINGN 54

OY 57 -----SPAPGR-----IAEVCVLRLEDELLEQIRPSVYRNVAROLHI 95

DB 55 PSWHLADSPAVNGATGSHSSSLDAREVYIPMAAVYKQALREAGDEPELRYRRASDLSLTSLHI 114  
 OY 96 PLOSEPVVDAFLAVAGHIFSGITMGKVVSLYSVAAGLAVDCVROAPAMVHALVDCIG 155  
 DB 115 ---TPGTAVOSFEQVAVNEJFRDGVNMGRIYAFEFSGALCVESVDKEMOVLVSKIASWMA 171  
 OY 156 EFVFKTLATWLRRRGCM 172  
 DB 172 TYLNDHLEPWIQENGCM 188

## RESULT 15

AAW01020 ID AAW01020 standard; Protein; 232 AA.

AC AAW01020;

DT 18-DEC-1996 (first entry)

DE Apoptosis-blocking protein Bcl-2 mutant 80-6 (del180-86).

KM Apoptosis-regulating protein; Bcl-2; oncogene;

KW adenovirus E1B 19K protein; cell death; cancer; tumour;

KM immune disorder; diagnosis; therapy; B1p1A; B1p13; B1p5; N1p1;

OS N1p2; N1p3.

PN Synthetic.

PD EP733706-A2.

PF 25-SEP-1996.

PR 21-MAR-1996; 96EP-0104542.

PA 21-MAR-1995; 95US-0408095.

PI (USL-) UNIV ST LOUIS.

DR Chinadural G;

DR WPI: 1996-427055/43.

PT Nucleic acids encoding apoptosis regulating proteins - useful for

PT diagnosing and treating immune disorders, malignancies, etc.

PS Example 8; Page 34-35; 60pp; English.

CC The 80-6 mutant (AAW01020) of the bcl-2 oncogene product (AAW01018)

CC lacks amino acids 80-86 of the native protein. This and other

CC Bcl-2 mutants (see also AAW01019-21) were used in a two hybrid assay

CC to examine the interactions between Bcl-2 and novel apoptosis-

CC regulating proteins N1p1, N1p2 and N1p3 (AAW00997-99). 2 Motifs

CC (AAW01003-04) on Bcl-2 were identified that are essential for

CC interaction with the Nip proteins. These motifs show homology

CC to motifs (AAW01005-06) identified on the adenovirus E1B 19K

CC apoptosis-blocking protein (AAW01010).

XX Sequence 232 AA;

XX Query Match 14.2%; Score 155; DB 17; Length 232;

XX Best Local Similarity 22.7%; Pred. No. 1.4e-08; Indels 46; Gaps 7;

XX Matches 46; Conservative 36; Mismatches 75; Indels 46; Gaps 7;

OY 37 EYVHARLRAGLSW-----SAPERASPARG-----GRLAECT-- 69

DB 17 KYTHYKLSQKGFSSNSDVENTEAPDEPEPEPERSAINGN 76

OY 70 -----VLRLEDELLEQIRPSVYRNVAROLHI-PLOSEPVVDAFLAVAGHIF 116

DB 77 APGSPVPVYVHLRLQAGDFSRRYRDRFAEMSSQLHLPFTAR-----GCFATVVEELFR 132

OY 117 AGITGWKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGFEVFKTLATWLRRRGCM 176

Db 133 DGVNNGRIVAFEFEGGVMCEVSNRMSPLVDNIALMTETYLNRHLHTWIODNGMDAFV 192  
Qy 177 KCV-VSTDGFRSHWL-VATLCS 197  
Db 193 ELYGPPMRPLFDPSMSEKTLIS 215

Search completed: April 29, 2003, 11:23:21  
Job time : 34.5339 secs

GenCore version 5.1.4-P5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:19:46 ; Search time 21.7493 seconds  
(without alignments)  
1610.532 Million cell updates/sec

Title: US-09-682-667-4  
Perfect score: 878  
Sequence: 1 MEVLRRSSVFYFAEIMDAFDR.....TLCSGRFLKAFLLPER 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	878	100.0	170	11	088857	088857 rattus norv
2	846.5	96.4	213	11	035425	035425 rattus norv
3	828.5	94.4	213	4	09UL32	09UL32 homo sapien
4	801	91.2	212	4	09UMX3	09UMX3 homo sapien
5	699.5	79.7	213	13	091812	091812 gallus gall
6	693.5	79.0	213	13	09DGS5	09DGS5 gallus gall
7	183	20.8	299	5	08TR8V	08TR8V drosophila
8	183	20.8	313	5	09NGX3	09NGX3 drosophila
9	173.5	19.8	247	5	09V612	09V612 drosophila
10	173	19.7	300	5	09V9C8	09V9C8 drosophila
11	142	16.2	317	5	095083	095083 drosophila
12	126.5	14.4	236	11	0923R6	0923R6 drosophila
13	109.5	12.5	192	13	0919M4	0919M4 brachydantio
14	109.5	12.5	219	11	099N36	099N36 mus musculu
15	109.5	12.5	235	11	035843	035843 mus musculu
16	107.5	12.2	238	13	090298	090298 brachydantio

17	105	12.0	180	6	Q9BDD5	Q9BDD5 bos taurus
18	105	12.0	188	11	Q9QWX2	Q9QWX2 mus musculu
19	105	12.0	217	11	Q9GNX3	Q9GNX3 mus musculu
20	105	12.0	233	11	Q35844	Q35844 mus musculu
21	104	11.8	233	6	Q9M257	Q9M257 ovis aries
22	104	11.8	233	6	Q9N1A2	Q9N1A2 sus scrofa
23	103	11.7	180	6	Q9BDX7	Q9BDX7 bos taurus
24	103	11.7	188	4	Q9H1R6	Q9H1R6 homo sapien
25	103	11.7	233	6	Q9MYW4	Q9MYW4 oryctolagus
26	103	11.7	233	6	Q8S042	Q8S042 felis silve
27	100	11.4	163	6	Q9M256	Q9M256 ovis aries
28	100	11.4	193	11	Q88996	Q88996 rattus norv
29	100	11.4	221	13	Q98U13	Q98U13 xenopus lae
30	99	11.3	204	13	Q902H2	Q902H2 xenopus lae
31	98	11.2	178	11	Q9CYW5	Q9CYW5 mus musculu
32	98	11.2	179	4	Q9NKG7	Q9NKG7 homo sapien
33	95	10.8	173	11	Q9UKL3	Q9UKL3 rattus norv
34	94.5	10.8	209	11	Q9UK59	Q9UK59 rattus norv
35	93	10.6	114	4	Q9NR76	Q9NR76 homo sapien
36	93	10.6	149	6	Q9GNG7	Q9GNG7 ovis aries
37	93	10.6	173	4	Q8W249	Q8W249 homo sapien
38	93	10.6	192	6	Q8S043	Q8S043 felis silve
39	91	10.4	172	11	Q55177	Q55177 mus musculu
40	90.5	10.3	182	16	Q8XUQ3	Q8XUQ3 raietonia s
41	87.5	10.0	172	11	Q55179	Q55179 mus musculu
42	86	9.8	175	11	Q925A9	Q925A9 rattus norv
43	85	9.7	308	17	Q8TX05	Q8TX05 methanopyru
44	82.5	9.4	412	16	Q9R135	Q9R135 streptomyce
45	80.5	9.2	860	16	Q9PEZ1	Q9PEZ1 xyella tas

## ALIGNMENTS

RESULT 1

088857 ID 088857 PRELIMINARY: PRT: 170 AA.

AC 088857: 01-NOV-1998 (TREMREL. 08, Created)

DT 01-NOV-1998 (TREMREL. 08, last sequence update)

DT 01-JUN-2002 (TREMREL. 21, last annotation update)

DE Bcl-2-related ovarian killer protein.

GN BOK.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=OVARY;

RX MEDLINE=98024143; PubMed=9356461;

RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;

RT "Bok is a pro-apoptotic bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic bcl-2 family members."

RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).

RL [2]

RN RP SEQUENCE FROM N.A.

RC TISSUE=OVARY;

RA Hsu S.Y., Hsueh A.J.W.;

RT "A splicing variant of the Bcl-2 member Bok with a truncated BH3 domain induces apoptosis without dimerization with anti-apoptotic Bcl-2 proteins."

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF051093; AAC61928.1; -

DR InterPro: IPR000712; Bcl2-BH.

DR InterPro: IPR002475; BCL2 family.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00337; BCL: 1.

DR PROSITE: PSS0062; BCL2\_FAMILY; 1.

SO SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

Query Match 100.0%; Score 878; DB 11; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.6e-74;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFSPPTDKELVAQAALGREYHARLRAGLSMSAPERASPAP 60  
DB 1 MEVLRRSSVFAAEIMDAFSPPTDKELVAQAALGREYHARLRAGLSMSAPERASPAP 60  
OY 61 GGRLAECTVLLRLGTTMGKVVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLA 120  
DB 61 GGRLAECTVLLRLGTTMGKVVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLA 120  
OY 121 TWLRRGGTVDLKCYSVTDPGFRSHMLVATLCSFGRFKAFFLLPPER 170  
DB 121 TWLRRGGTVDLKCYSVTDPGFRSHMLVATLCSFGRFKAFFLLPPER 170

## RESULT 2

035425 PRELIMINARY; PRT; 213 AA.

AC 035425;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE BCL-2-related ovarian killer protein.  
GN BOK OR BOKL OR BOK OR MTD.  
OS Rattus norvegicus (Rat), and  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116, 10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat; STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, AND UTERUS;  
RX MEDLINE=98024143; PubMed=9356461;  
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
RT "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in  
reproductive tissues and heterodimerizes with selective anti-apoptotic  
Bcl-2 family members";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat; STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, AND UTERUS;  
RA Hsu S.Y., Hsueh A.J.W.;  
RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Mouse;  
RA Inohara N., Ekhterae D., Garcia I., Carrio R., Merino J., Merry A.,  
Chen S., Nunez G.;  
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF027954; AAB87418.1; -;  
DR EMBL; AF027707; AAC53582.1; -;  
DR MGI; MGI:1858494; Bok.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
SQ SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

Query Match 96.4%; Score 846.5; DB 11; Length 213;  
Best Local Similarity 79.8%; Pred. No. 1.8e-71;  
Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;  
OY 1 MEVLRRSSVFAAEIMDAFSPPTDKELVAQAALGREYHARLRAGLSMSAPERASPAP 60  
DB 1 MEVLRRSSVFAAEIMDAFSPPTDKELVAQAALGREYHARLRAGLSMSAPERASPAP 60  
OY 61 GGRLAECTVLLRLGTTMGKVVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLA 120  
DB 61 GGRLAECTVLLRLGTTMGKVVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLA 120  
OY 121 TWLRRGGTVDLKCYSVTDPGFRSHMLVATLCSFGRFKAFFLLPPER 170  
DB 121 TWLRRGGTVDLKCYSVTDPGFRSHMLVATLCSFGRFKAFFLLPPER 170

DB 121 WCKVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLATWLRGGTVDLKCYY 180

OY 138 STDPGFRSHMLVATLCSFGRFKAFFLLPPER 170  
DB 181 STDPGFRSHMLVATLCSFGRFKAFFLLPPER 213

## RESULT 3

09UL32 PRELIMINARY; PRT; 213 AA.

AC 09UL32;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE BCL-2 related ovarian killer.  
GN BOK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homd.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "CDNA cloning of the human Bok gene";  
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF089746; AAF09129.1; -;  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
SQ SEQUENCE 213 AA; 23540 MW; 59509F8C7330517F CRC64;

Query Match 94.4%; Score 828.5; DB 4; Length 213;  
Best Local Similarity 78.4%; Pred. No. 8.6e-70;  
Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

OY 1 MEVLRRSSVFAAEIMDAFSPPTDKELVAQAALGREYHARLRAGLSMSAPERASPAP 60  
DB 1 MEVLRRSSVFAAEIMDAFSPPTDKELVAQAALGREYHARLRAGLSMSAPERASPAP 60  
OY 61 GGRLAECTVLLRLGTTMGKVVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLA 120  
DB 61 GGRLAECTVLLRLGTTMGKVVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLA 120  
OY 78 WCKVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLATWLRGGTVDLKCYY 137  
DB 121 WCKVSLYSVAGLAVDCVROAOPAMVHALVDCIGEFVKTLLATWLRGGTVDLKCYY 180  
OY 138 STDPGFRSHMLVATLCSFGRFKAFFLLPPER 170  
DB 181 STDPGFRSHMLVATLCSFGRFKAFFLLPPER 213

## RESULT 4

09UMX3 PRELIMINARY; PRT; 212 AA.

AC 09UMX3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE BCL-2-related ovarian killer protein (Similar to BCL-2-related ovarian  
killer protein-like-PENDING) (BCL-2-related ovarian killer  
protein-like).  
GN BOK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang H.;

RT "Gene expression of a human homolog of BCL-2-related ovarian killer protein.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MUSCLE;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MUSCLE;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF174487; AAD51719.1; -  
 DR EMBL; BC006203; AAH06203.1; -  
 DR EMBL; BC017214; AAH17214.1; -  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 212 AA; 23280 MW; 053ED05FE8E5B2 CRC64;

Query Match 91.2%; Score 801; DB 4; Length 212;  
 Best Local Similarity 76.1%; Pred. No. 3.2e-67;  
 Matches 162; Conservative 3; Mismatches 4; Indels 44; Gaps 2;

OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSASAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSASAPERASAP 60  
 OY 61 GGRLAECVTVLRL-----GTP 77  
 DB 61 -GRLAEVCATLLRLGDELEYIRPNVYRNARQLNISLHSEVTVDALFAVAQIFTAGIT 119  
 OY 78 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCGFEVTKTLTWLRRGGMTDYLKCV 137  
 DB 120 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCGFEVTKTLTWLRRGGMTDYLKCV 179  
 OY 138 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 170  
 DB 180 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 212

RESULT 5  
 OY 091812 PRELIMINARY; PRT; 213 AA.  
 AC 091812;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE Bcl-2-related ovarian killer protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487164; PubMed=11034351;  
 RA Zhang H., Holzgrevé W., De Geyter C.;  
 RT Evolutionarily conserved Bcl proteins in the Bcl-2 family.";  
 RL FEBS Lett. 480:311-313(2000).  
 DR EMBL; AF275944; AAF81282.1; -  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23619 MW; B3AF7049F25442E3 CRC64;

Query Match 79.7%; Score 699.5; DB 13; Length 213;  
 Best Local Similarity 62.9%; Pred. No. 1e-57;

Matches 134; Conservative 18; Mismatches 18; Indels 43; Gaps 1;  
 OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSASAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSASAPERASAP 60  
 OY 61 GGRLAECVTVLRL-----GTP 77  
 DB 61 GGRLAECVTVLRL-----GTP 77  
 OY 78 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCGFEVTKTLTWLRRGGMTDYLKCV 137  
 DB 121 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCGFEVTKTLTWLRRGGMTDYLKCV 180  
 OY 138 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 170  
 DB 181 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 213

RESULT 6  
 OY 09DGJ5 PRELIMINARY; PRT; 213 AA.  
 AC 09DGJ5;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE Bcl-2-related ovarian killer protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Millis E.M., Johnson A.L., Bridgman J.T.;  
 RT Characterization and Expression of Bcl in the Hen Ovary.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF290888; AAG01182.1; -  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23658 MW; 07CC06BBD7311EC CRC64;

Query Match 79.0%; Score 693.5; DB 13; Length 213;  
 Best Local Similarity 62.0%; Pred. No. 3.7e-57;  
 Matches 132; Conservative 19; Mismatches 19; Indels 43; Gaps 1;  
 OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSASAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSASAPERASAP 60  
 OY 61 GGRLAECVTVLRL-----GTP 77  
 DB 61 GGRLAECVTVLRL-----GTP 77  
 OY 78 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCGFEVTKTLTWLRRGGMTDYLKCV 137  
 DB 121 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCGFEVTKTLTWLRRGGMTDYLKCV 180  
 OY 138 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 170  
 DB 181 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 213

RESULT 7  
 OY 08T8Y5 PRELIMINARY; PRT; 299 AA.  
 AC 08T8Y5;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

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DE AT16536P.
GN BUFFY.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Abdayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Patagas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY075219; AAL68086.1; -.
SQ SEQUENCE 299 AA: 33379 MW: 7PB125A6B332B23 CRC64;

Query Match 20.8%; Score 183; DB 5; Length 299;
Best Local Similarity 26.9%; Pred. No. 3e-09;
Matches 56; Conservative 26; Mismatches 60; Indels 66; Gaps 8;

OY 25 KETVAQAKALGREYVHARLLRAGL-----SWGAP----- 53
DB 87 ODIISQGRCLGCHYIKRRLRSGLFNKKIGLQIRISLSTSMGIVRDVFPVAVYGLDEL 146
OY 54 ERASPA-----PGGR-----LAECVTLRLGITWGVSLYSVAGL 91
DB 147 ERMHRIYNGVARQICRNNGGFEHPDVAVSLLGAVGRELFVEITWKSVISLFAIAGL 206
OY 92 AVDCVRQAPAVVHALVDCLGFEVFKTLATWLRRGGW---TDVLKCVSTDPGFRSHW 147
DB 207 SYDCVRQGHPEYLPKLMEVSEVIEDVLPWLNENGWSGINTHVLPTTNSLNP---LEW 263
OY 148 LVATL-CSFG-----RFLKAFELLPE 169
DB 264 TTLVIGVVFGLLVFMILFRIFNLIVPK 291

RESULT 8
O9NGX3 PRELIMINARY: PRT: 313 AA.
AC O9NGX3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-2-like protein BUFFY (Fragment).
OS Drosophila melanogaster (Fruit fly).
GN BUFFY OR CG8238.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20153510; PubMed=10684252;
RA Colussi P.A., Quinn L.M., Huang D.C., Coombe M., Read S.H.,
RA Richardson H., Kumar S.;
DE Bcl-2, a proapoptotic bcl-2 homologue, is a component of the
RL Drosophila melanogaster cell death machinery.
RT J. Cell Biol. 148:703-714(2000).
DR EMBL: AF237864; AAF44120.1; -.
DR HSSP: Q07817; 1MAZ.
DR FLYBase: FBgn0040491; BUffy.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2_1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PS50062; BCL2_FAMILY_1.
FT NON_TER 1
SQ SEQUENCE 313 AA: 34909 MW: 775AA1FDD5B678E CRC64;

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Query Match 20.8%; Score 183; DB 5; Length 313;
Best Local Similarity 26.9%; Pred. No. 3.2e-09;
Matches 56; Conservative 26; Mismatches 60; Indels 66; Gaps 8;

OY 25 KETVAQAKALGREYVHARLLRAGL-----SWGAP----- 53
DB 101 ODIISQGRCLGCHYIKRRLRSGLFNKKIGLQIRISLSTSMGIVRDVFPVAVYGLDEL 160
OY 54 ERASPA-----PGGR-----LAECVTLRLGITWGVSLYSVAGL 91
DB 161 ERMHRIYNGVARQICRNNGGFEHPDVAVSLLGAVGRELFVEITWKSVISLFAIAGL 220
OY 92 AVDCVRQAPAVVHALVDCLGFEVFKTLATWLRRGGW---TDVLKCVSTDPGFRSHW 147
DB 221 SYDCVRQGHPEYLPKLMEVSEVIEDVLPWLNENGWSGINTHVLPTTNSLNP---LEW 277
OY 148 LVATL-CSFG-----RFLKAFELLPE 169
DB 278 TTLVIGVVFGLLVFMILFRIFNLIVPK 305

RESULT 9
O9V612 PRELIMINARY: PRT: 247 AA.
AC O9V612:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG8238 protein.
OS Drosophila melanogaster (Fruit fly).
GN BUFFY OR CG8238.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McShenel D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Koshnell A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon R., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheelers F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW DNA-binding; zinc-finger.  
 FT CONFLICT 1 86 MISSING (IN REF. 4).  
 FT CONFLICT 215 215 I->V (IN REF. 1).  
 FT CONFLICT 217 217 C->R (IN REF. 4).  
 SO SEQUENCE 300 AA; 32940 MW; FF29E0ADCFF3D0942 CRC64;

Query Match 19.7%; Score 173; DB 5; Length 300;  
 Best Local Similarity 28.2%; Pred. No. 2.6e-08;  
 Matches 44; Conservative 17; Mismatches 43; Indels 52; Gaps 3;

OY 26 ELVQAQKALGRYVHARLRAG-LSMSAPER-----VCTVLLRLGITWGVKVSLSVAAGLAV 93  
 DB 96 DIINGKCLCGYIRARRRAGVLRNRYQLRNILDPGSSHVYVEVPALNSMGEELER 155  
 OY 56 -----ASPAPGRLAE-----VCTVLLRLGITWGVKVSLSVAAGLAV 93  
 DB 156 MHPRYTINISROLSPAPGGELESDMAPMLNLVAKDLFRSSITWGIITIFAVCGGFAT 215  
 OY 94 DCVROQAPAMVHALVDCIGEEFVRK--TLATWLRRRG 129  
 DB 216 DCVROGHFDYDGLDGLAEITEDLVYVLDINGM 251

## RESULT 11

O95083 PRELIMINARY; PRT; 317 AA.

ID O95083  
 AC O95083  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GH01265P.  
 GN DEBCL OR CG12397.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
 RL Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY058249; AAL13478.1; -.  
 DR FlyBase: FBgn0029131; debcl.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 SO SEQUENCE 317 AA; 34649 MW; 46B22FED1CC6F01F CRC64;

Query Match 16.2%; Score 142; DB 5; Length 317;  
 Best Local Similarity 27.4%; Pred. No. 2.2e-05;  
 Matches 43; Conservative 18; Mismatches 42; Indels 54; Gaps 4;

OY 26 ELVQAQKALGRYVHARLRAG-LSMSAPER-----VCTVLLRLGITWGVKVSLSVAAGLAV 93  
 DB 96 DIINGKCLCGYIRARRRAGVLRNRYQLRNILDPGSSHVYVEVPALNSMGEELER 155  
 OY 56 -----ASPAPGRLAE-----VCTVLLRLGITWGVKVSLSVAAGLAV 93  
 DB 156 MHPRYTINISROLSPAPGGELESDMAPMLNLVAKDLFRSSITWGIITIFAVCGGFAT 215  
 OY 94 DCVROQAPAMVHALVDCIGEEFVRK--TLATWLRRRG 128  
 DB 216 DCVROGHFDYDGLDGLAEITEDLVYVLDINGM 252

RESULT 12  
 O923R6  
 ID O923R6 PRELIMINARY; PRT; 236 AA.  
 AC O923R6  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B-cell lymphoma protein 2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
 OX NCBI\_TaxID=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Lai D.Z., Chen W., Wang H.T.;  
 RT "Construction of a robust CHO cell line for biopharmaceutical use."  
 RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF04339; AAK92201.1; -.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_family.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
 DR PROSITE: PS01259; BH3; UNKNOWN\_1.  
 DR PROSITE: PS01260; BH4\_1; UNKNOWN\_1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 SO SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match 14.4%; Score 126.5; DB 11; Length 236;  
 Best Local Similarity 18.9%; Pred. No. 0.00045;  
 Matches 40; Conservative 25; Mismatches 36; Indels 91; Gaps 4;

OY 28 VAQAKALG-----REYVHARLRAGLSW-----SAPERASAPAG-----61  
 DB 1 MAQAGRTGVDNREIYMKYIHYKLSRGYEMDGDVDAAPLGAAPRGJFSPGSPNPRA 60  
 OY 62 -----61  
 DB 61 VHRDMAARTSPRLPVATGPTLSPVPVHLTLRRAGDDESRRYRDPFAEMSSQLHTLP 120  
 OY 62 -----GLAEVCVLLRLGITWGVKVSLSVAAGLAVDCVROQAPAMVHALVDCIGEEFVRK 117  
 DB 121 FTARGRFATVVEELFRDGVNMGRIYAFEPFGVCWCESVNRMSPLVDNIALMTEYLNR 180  
 OY 118 TLATWLRRRGVTDVLCV-VSTDGPFRRHWL 148  
 DB 181 HHTWIDONGMDAFVELYGPVRLPDPFSL 212

## RESULT 13

O919N4 PRELIMINARY; PRT; 192 AA.

ID O919N4  
 AC O919N4  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bax.  
 GN BAX.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RX MEDLINE-20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
   zebrafish."
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF231015; AAF69650.1; -.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL.1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 192 AA; 21401 MW; 8A71A630A56FDC32 CRC64;

Query Match 12.5%; Score 109.5; DB 13; Length 192;
Best Local Similarity 21.0%; Pred. No. 0.014;
Matches 34; Conservative 29; Mismatches 64; Indels 35; Gaps 4;

OY 6 NSSVFAEIMDAFDRSPDKELVAQAKALGREYVHARLLRAGLSWAPERASPARGRILA 65
DB 45 RSQLGVEICD-----PSHKRLAQCLQIQIDELDGNAGLSMLN-----NSNIQ 88
OY 66 EVCYVLLRLG-----ITWGVSLKSVAGLAVDCVROQAPAMVHALVDCIGFVRK 117
DB 89 PTQDFIRVAREIFSDGKFMGRVVALFEACRLVKAISTRVPIIRTIIISWTMSYIOE 148
OY 118 TLATWLRRRGWTDLKCVSTDPGFRSHMLVATLCSEGRFL 159
DB 149 HYINMIREGGW-----DGIRSFYGTPTQVTVFL 179

RESULT 14
O99N36 PRELIMINARY; PRT; 219 AA.
ID O99N36;
AC O99N36;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE B-cell leukemia/lymphoma x-gamma (Fragment).
GN BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Yang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
   gene Bcl-x-gamma."
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF133279; AAK15454.1; -.
DR EMBL; AF133281; AAK15454.1; JOINED.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL.1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
FT NON_TER
SQ SEQUENCE 219 AA; 24224 MW; EB352ECACFAA6AF5 CRC64;

Query Match 12.5%; Score 109.5; DB 11; Length 219;
Best Local Similarity 25.0%; Pred. No. 0.016;
Matches 25; Conservative 17; Mismatches 43; Indels 15; Gaps 3;

OY 66 EVCYVLLRLGITWGVSLKSVAGLAVDCVROQAPAMVHALVDCIGFVRKTLATWLR 125
DB 109 QVNNELFRDGVNMGRIVAFESFGALCVESVDKEMQVLVSRIASMMATYLNHLEPWIOE 168
OY 126 RCGW-----TDVLKCVSTDPGFRSH-----WLVAT 151

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DB 169 NCGWGVSGGTPLRSVFRRLVQV-PGVAEHVCDPSLWEVET 207
RESULT 15
O35843 PRELIMINARY; PRT; 235 AA.
ID O35843;
AC O35843;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-x-gamma.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=THYMUS;
RX MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
   apoptosis in T cells."
RL Immunity 7:629-639(1997).
DR EMBL; U51277; AAC53458.1; -.
DR HSSP; P53563; IAF3.
DR MGI; MGI:88139; Bcl2L.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL.1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;

Query Match 12.5%; Score 109.5; DB 11; Length 235;
Best Local Similarity 25.0%; Pred. No. 0.017;
Matches 25; Conservative 17; Mismatches 43; Indels 15; Gaps 3;

OY 66 EVCYVLLRLGITWGVSLKSVAGLAVDCVROQAPAMVHALVDCIGFVRKTLATWLR 125
DB 125 QVNNELFRDGVNMGRIVAFESFGALCVESVDKEMQVLVSRIASMMATYLNHLEPWIOE 184
OY 126 RCGW-----TDVLKCVSTDPGFRSH-----WLVAT 151
DB 185 NCGWGVSGGTPLRSVFRRLVQV-PGVAEHVCDPSLWEVET 223

```

Search completed: April 29, 2003, 11:25:40  
 Job time : 22.7493 secs



GenCore version 5.1.4p5\_4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 5.99217 Seconds

(without alignments)  
1176.639 Million cell updates/sec

Title: US-09-682-667-4

Perfect score: 878

Sequence: 1 MEVLRRSSVFPAEIMDAFDR.....TLCSFGRLKAFLLPER 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	15.6	236	1 BCL2_RAT	P49950 ratu
2	130	14.8	239	1 BCL2_HUMAN	P10415 hom
3	129	14.7	229	1 BCL2_BOVIN	O02718 bos
4	128	14.6	236	1 BCL2_CRITO	O91417 mus
5	127	14.5	236	1 BCL2_MOUSE	P10417 mus
6	113	12.9	233	1 BCL2_CHICK	O00709 gall
7	110	12.5	228	1 ARL_XENLA	O91827 xen
8	107	12.2	233	1 BCLX_RAT	P53563 ratu
9	105.5	12.0	229	1 BCLX_CHICK	O07816 gall
10	105	12.0	233	1 BCLX_MOUSE	O64373 mus
11	104	11.8	233	1 BCLX_PIG	O77737 sus
12	103	11.7	233	1 BCLX_HUMAN	O07817 hom
13	101	11.5	218	1 BAXB_HUMAN	O07814 hom
14	100	11.4	193	1 BCLM_MOUSE	P70345 mus
15	99	11.3	204	1 ARL1_XENLA	O91828 xen
16	97	11.0	211	1 BAK_HUMAN	O07811 hom
17	96	10.9	192	1 BAXA_HUMAN	O07812 hom
18	96	10.9	193	1 BCLM_HUMAN	O92843 hom
19	95	10.8	192	1 BAXA_MOUSE	O07813 mus
20	95	10.8	192	1 BAXA_MOUSE	O07813 mus
21	94	10.7	208	1 BAK_MOUSE	O08390 ratu
22	93.5	10.6	143	1 BAXD_HUMAN	O02703 bos
23	93	10.6	192	1 BAXA_BOVIN	O02703 bos
24	87	9.9	211	1 BAK2_HUMAN	O13014 hom
25	83.5	9.5	172	1 BFL1_MOUSE	O07440 mus
26	80	9.1	535	1 SSOH_HUMAN	P51849 hom
27	80	9.1	1115	1 CARB_MYCTU	P57689 myc
28	79	9.0	401	1 PILC_PSEPU	P36641 pseu
29	78	8.9	175	1 BFL1_HUMAN	O16548 hom
30	76.5	8.7	297	1 NADC_HUMAN	O15274 hom
31	75.5	8.6	610	1 RHO_MYCLE	P45835 myc
32	75.5	8.6	1705	1 PTPD_MOUSE	P70289 myc
33	75	8.5	1300	1 IRR_MOUSE	O9wcl14 mus

34	74.5	8.5	602	1 RHO_MYCTU	O10607 myc
35	74.5	8.5	728	1 VIV_ORYSA	P37398 crya
36	73.5	8.4	350	1 MCIL_HUMAN	O07820 hom
37	73	8.3	378	1 MYI2_MYCTU	O10400 myc
38	72.5	8.3	177	1 NR13_COTJA	O90343 cotu
39	72.5	8.3	539	1 TCP2_CAEL	P46550 caen
40	72.5	8.3	1557	1 DVAL_DICVI	O24702 dicv
41	72	8.2	370	1 IDI2_PYRAB	O9u259 pyro
42	72	8.2	517	1 CRT1_MYXXA	P54879 myxo
43	71.5	8.1	438	1 Y485_MYCTU	O11151 myc
44	71.5	8.1	1121	1 CARB_MYCLE	O9ccr2 myc
45	71	8.1	288	1 FIXA_BRAVA	P53577 brady

## ALIGNMENTS

RESULT 1	ID	Accession	Standard	PRT	236 AA
BCL2_RAT	AC	P49950	062837	064032	
BCL2_RAT	AC	P49950	062837	064032	
01-OCT-1996 (Rel. 34, Created)	DT	01-NOV-1997 (Rel. 35, Last sequence update)			
15-JUN-2002 (Rel. 41, Last annotation update)	DT				
Apoptosis regulator Bcl-2.	DE				
BCL2 OR BCL-2.	GN				
Rattus norvegicus (Rat).	OS				
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	OC				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	OX				
NCBI_Taxid=10116;	OX				
SEQUENCE FROM N.A.	RP				
TISSUE=Brain;	RC				
MEDLINE=94193015; PubMed=8144041;	RX				
Sato T., Irie S., Królowski S., Reed J.C.;	RA				
"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";	RT				
Gene 140:291-292(1994).	RL				
SEQUENCE FROM N.A.	RP				
STRAIN=Sprague-Dawley; TISSUE=Ovary;	RC				
MEDLINE=95129487; PubMed=7828536;	RX				
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;	RA				
"Expression of members of the bcl-2 gene family in the immature rat	RT				
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa	RT				
cell apoptosis is associated with decreased bax and constitutive	RT				
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";	RT				
Endocrinology 136:232-241(1995).	RL				
SEQUENCE OF 19-172 FROM N.A.	RP				
MEDLINE=95059917; PubMed=7969891;	RX				
Castren E., Ohga Y., Bertzagh M.P., Tsimogiorgis G., Thoenen H.,	RA				
Lindholm D.;	RT				
"bcl-2 messenger RNA is localized in neurons of the developing and	RT				
adult rat brain.";	RT				
Neuroscience 61:165-177(1994).	RL				
-1- FUNCTION: Suppresses apoptosis in a variety of cell systems	CC				
including factor-dependent lymphohematopoietic and neural cells.	CC				
Regulates cell death by controlling the mitochondrial membrane	CC				
permeability. Appears to function in a feedback loop system with	CC				
caspases. Inhibits caspase activity either by preventing the	CC				
release of cytochrome c from the mitochondria and/or by binding to	CC				
the apoptosis-activating factor (APAF-1).	CC				
-1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and	CC				
Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2	CC				
domains, and is necessary for anti-apoptotic activity (By	CC				
similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).	CC				
-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular	CC				
membrane of the nuclear envelope and the endoplasmic reticulum.	CC				
-1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with	CC				
highest levels in reproductive tissues. In the adult brain,	CC				
expression is localized in mitral cells of the olfactory bulb,	CC				
granular and pyramidal neurons of hippocampus, pontine nuclei,	CC				
cerebellar granule neurons, and in ependymal cells. In prenatal	CC				



RT apoptosis and heterodimerization with Bax.";  
 RL Nature 369:321-323(1994).  
 RN [8]  
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
 RX MEDLINE-98057466; PubMed-9395403;  
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
 RA Ueno K., Hardwick J.M.;  
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";  
 RL Science 278:1966-1988(1997).  
 RN [9]  
 RP REVIEW ON PHOSPHORYLATION.  
 RX MEDLINE-21260650; PubMed-11368354;  
 RA Ruvolo P.P., Deng X., May W.S.;  
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";  
 RL Leukemia 15:515-522(2001).  
 RN [10]  
 RP PHOSPHORYLATION BY ASK1/JNK1.  
 RX MEDLINE-20036804; PubMed-10567572;  
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
 RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
 RT protein kinase pathway normally activated at G(2)/M.";  
 RL Mol. Cell. Biol. 19:8469-8478(1999).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(l). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAf-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAf-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- DEPHOSPHORYLATED BY protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type  
 CC II chronic lymphatic leukemia) by a chromosomal translocation  
 CC t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene  
 CC regions.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;  
 CC WWW-"http://www.infobiogen.fr/services/chronocancer/Genes/BCL2ID49.html".  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to license@sib-sib.ch).  
 DR EMBL: M13994; AAA51813.1; ALT\_SEQ.  
 DR EMBL: M13995; AAA51814.1; ALT\_SEQ.

DR EMBL: M1745; AAA55591.1; -;  
 DR EMBL: X06487; CAA29778.1; -;  
 DR EMBL: S72602; AAD14111.1; ALT\_SEQ.  
 DR PIR: A29409; TVHDA1.  
 DR PIR: B29409; TVHDA1.  
 DR PIR: A24428; TVHDA1.  
 DR PIR: C37332; C37332.  
 DR PIR: D37332; D37332.  
 DR HSSP: 007817; 1MAZ.  
 DR Genew: HGNC:990; BCL2.  
 DR MIM: 151430; -;  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMS: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS50063; BH4.2; 1.  
 KW Proto-oncogene; Apoptosis; BCL2; 1.  
 KW Mitochondrion; Phosphorylation; Alternative splicing; Transmembrane;  
 KW Polymorphism; Disease mutation.  
 KW Polyorphism; Disease mutation.  
 FT DOMAIN 10 30  
 FT DOMAIN 93 107  
 FT DOMAIN 136 155  
 FT DOMAIN 187 202  
 FT TRANSMEM 212 233  
 FT SITE 34 35  
 FT MOD\_RES 70 70  
 FT VARSPPLIC 196 239  
 FT VARIANT 7 7  
 FT FT 7 7  
 FT VARIANT 59 59  
 FT FT 59 59  
 FT VARIANT 93 93  
 FT FT 93 93  
 FT VARIANT 34 34  
 FT MUTAGEN 64 64  
 FT MUTAGEN 145 145  
 FT FT 188 188  
 FT MUTAGEN 48 48  
 FT CONFLICT 59 59  
 FT CONFLICT 117 117  
 FT CONFLICT 129 129  
 SQ SEQUENCE 239 AA; 26266 MW; 3C49F2B714DC9CBB CRC64;  
 Query Match 14.8%; Score 130; DB 1; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 1.3e-05;  
 Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;  
 QY 37 EYVHARLLRAGLSM-----SAPERASPARC----- 61  
 DB 17 KYTHKLSQNGYEMDAGVGAAPGAPAGITSSQPGHPRHRAASDPARTSPLOTPTA 76  
 QY 62 -----GRLAEYCTV 70  
 DB 77 APCAAGPALSPVPVYVHLTLRQAGDEFSRRYRRDFAEKSSQLHLPTFARGFATVVEE 136  
 QY 71 LFLGLITWGVVSLYSVAGLAVDCYRQAPAAVYHALVCLGFFVKTKLATWLRRGGW 130  
 DB 137 LFRDGVNCRIVAFPEGGVGVESVNRKMSPLVDNIALIMWTEYLNRHLHTWIDNGMD 196

QY 131 DYKCV-VSTDPEFSHWL-VATLCS 154  
 DB 197 AFVELGPSMRPLDFESWLSLTKLLS 222

RESULT 3  
 BCL2\_BOVIN STANDARD: PRT: 229 AA.

AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=Thymus;  
 RA Reyes R.A., Cockrell G.L.;  
 RT "Bovine leukemia virus associated leukemogenesis is correlated  
 with suppression of programmed cell death and increased expression  
 of Bcl-2.";  
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 permeability. Appears to function in a feedback loop system with  
 caspases. Inhibits caspase activity either by preventing the  
 release of cytochrome c from the mitochondria and/or by binding to  
 the apoptosis-activating factor (APAF-1) (By similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 domains, and is necessary for anti-apoptotic activity (By  
 similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 membrane of the nuclear envelope and the endoplasmic reticulum (By  
 similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 for interaction with RAIF-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 on Ser-70 by PKC is required for the anti-apoptosis activity and  
 occurs during the G2/M phase of the cell cycle (By similarity). In  
 the absence of growth factors, Bcl2 appears to be phosphorylated  
 by other protein kinases such as ERKs and stress-activated  
 kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
 similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 activity, causes the release of cytochrome c into the cytosol  
 promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

-----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL: U92434; AAB53319.1;  
 DR HSSP: 007817; IMAZ;  
 DR InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30  
 FT DOMAIN 64 68 POLY-PRO.  
 FT DOMAIN 69 72 POLY-ALA.  
 FT DOMAIN 83 97 BH3.  
 FT DOMAIN 126 145 BH1.  
 FT DOMAIN 177 192 BH2.  
 FT TRANSMEM 202 223 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD\_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 SQ SEQUENCE 229 AA: 25099 MW: ADIDDOAF98FFFIID CRC64;

Query Match 14.7%; Score 129; DB 1; Length 229;  
 Best Local Similarity 19.7%; Pred. No. 1.5e-05;  
 Matches 41; Conservative 25; Mismatches 56; Indels 86; Gaps 4;

QY 37 EYVHALLACLSW-----SAPERSAPAG----- 61  
 DB 17 KTHVKSORGTEWDAGDAGAPGAPAGILSSOPRTAPSRTPPPPAAGAP 76  
 QY 62 -----GLAEVCTVLRIGTWCK 80  
 DB 77 SPVPVHILTLQAGDGFRRYRDRFAEMSQLHLPTAREFAVVELEFRDGMGR 136  
 QY 81 VSLSVANGADVCRQAPMVAHVDLGEFVKTLATWLRRGGTVDYKCV-VST 139  
 DB 137 IVAFFEGGVMCEVSYNREMSPLVDISIALMTEYLNRHLHTWIDNGDAVEVLGSPM 196

QY 140 DGFRRSHWLVAATLCSGRFLKAAFFLL 167  
 DB 197 RPLDFESWL-----SLKALLSLAL 215

RESULT 4  
 BCL2\_CRITLO STANDARD: PRT: 236 AA.

AC 09JUV8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
 OX NCBI\_TaxID=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=20431763; PubMed=10973819;  
 RA Tomicic M.T., Christmann M., Kaina B.;  
 RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2  
 protein.";  
 RL Biochem. Biophys. Res. Commun. 275:899-903(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.  
 RX MEDLINE=21092839; PubMed=11181062;  
 RA Tomicic M.T., Kaina B.;



```

RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT and caspase-3."
CC RT. Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAf-1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAf-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC (By similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
CC EMBL: AJ271720; CAB92245.1; -.
CC DR HSSP: Q07817; IMAZ.
CC DR InterPro: IPR002475; BCL2_family.
CC DR InterPro: IPR000712; BCL2_BH.
CC DR InterPro: IPR003093; BCL2_BH4.
CC DR InterPro: IPR004725; BCL2_reg.
CC DR Pfam: PF00452; Bcl-2; 1.
CC DR Pfam: PF02180; BCL; 1.
CC DR SMART: SM00337; BCL; 1.
CC DR SMART: SM00265; BH4; 1.
CC DR TIGRfams: TIGR00865; bcl-2; 1.
CC DR PROSITE: PS50062; BCL2_FAMILY; 1.
CC DR PROSITE: PS01080; BH1; 1.
CC DR PROSITE: PS01258; BH2; 1.
CC DR PROSITE: PS01259; BH3; 1.
CC DR PROSITE: PS01260; BH4_1; 1.
CC DR PROSITE: PS50063; BH4_2; 1.
CC DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
CC KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
CC FT DOMAIN 10 30 BH4.
CC FT DOMAIN 90 104 BH3.
CC FT DOMAIN 133 152 BH1.
CC FT DOMAIN 184 199 BH2.
CC FT TRANSMEM 209 230 BH2.
CC FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
CC FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
CC SQ SEQUENCE 236 AA; 26491 MW; BECADPIEF3337228 CRC64;
Query Match 14.6%; Score 128; DB 1; Length 236;
Best Local Similarity 19.6%; Pred. No. 1.9e-05;

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Matches 43; Conservative 26; Mismatches 58; Indels 92; Gaps 5;
QY 28 VAQAKALG-----REYVHARILRAGLSW-----SAPERASAPG----- 61
Db :||| | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
1 MAQGRGTGYNDREIWMYIHKLSQRYEMDVGVDYAPAGAAFTPGIFSPESNPTPA 60
QY 62 ----- 61
Db 61 VHRMARSPRLPRIVATGTGPTLSPPVPVHLTLRRAGDDFSRRYRRDPAEMSQHLTP 120
QY 62 ----GRAEYCVTLRLGITWGWKVSLSVAAGLAVDCRQADPAMVHALVDCIGFVRK 117
Db :||| | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
121 FTARGFATVVEELFRDGVWGRIVAFEEFGVGCVSVREMSPLVDNALMTETYLNR 180
QY 118 TLATLRRRGGMVTLKCV--VSTDGGRSHML-VATICS 154
Db :||| | :||: | :||: | :||: | :||: | :||: | :||: | :||: |
181 HLHTWIDNGGMDAFELVGYSPRPLPFDPSWLSKLTLIS 219
RESULT 5
BCL2_MOUSE STANDARD; PRT; 236 AA.
ID BCL2_MOUSE
AC P10417; P10418;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC SRRAIN-BALB/C; TISUP-Liver.
RX MEDLINE=87187643; PubMed=303245;
RA Negri M., Sili M., Kozak C., Tsujimoto Y., Croce C.M.;
RT "Molecular analysis of mcl-2: structure and expression of the murine
RL gene homologous to the human gene involved in follicular lymphoma.";
RL Cell 49:455-463(1987).
RL [2]
RP REVISIONS TO 221-222.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguich Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RL in a variety of tissues including lymphoid and neuronal organs in
RL adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RL [3]
RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=92727291; PubMed=9115213;
RA Ito T., Deng X., Carr B., May W.S. Jr.;
RT "bcl-2 phosphorylation required for anti-apoptosis function.";
RL J. Biol. Chem. 272:11671-11673(1997).
RL [4]
RP DEPHOSPHORYLATION BY PP2A.
RX MEDLINE=99069407; PubMed=9852076;
RA Deng X., Ito T., Carr B., Mumby B., May W.S. Jr.;
RT "Reversible phosphorylation of Bcl2 following interleukin 3 or
RL bryostatins 1 is mediated by direct interaction with protein
RL phosphatase 2A*.";
RL J. Biol. Chem. 273:34157-34163(1998).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAf-1.

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RA SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
 RC TISSUE-Brain;  
 RA Michaelidis T.M.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RA Messelink S.L., David G.L., Choi S., Velluona M., Hardwick J.M.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).  
 RC TISSUE-Thymus;  
 RA MEDLINE=96278736; PubMed=8662675;  
 RA Shiralwa N., Inohara N., Okada N., Yuzaki M., Shoji S.-I., Ohta S.;  
 RT "An additional form of rat Bcl-x, Bcl-xdelta, generated by an  
 RT unspliced RNA, promotes apoptosis in promyeloid cells.";  
 RL J. Biol. Chem. 271:13258-13265(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
 RC STRAIN-Sprague-Dawley; TISSUE-Ovary;  
 RA MEDLINE=95129487; PubMed=7828536;  
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
 RT "Expression of members of the bcl-2 gene family in the immature rat  
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
 RT cell apoptosis is associated with decreased bax and constitutive  
 RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";  
 RL Endocrinology 136:232-241(1995).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RA MEDLINE=98010630; PubMed=9346936;  
 RA Artion M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,  
 RA Morikawa K.;  
 RT "Crystal structure of rat Bcl-XL. Implications for the function of  
 RT the Bcl-2 protein family.";  
 RL J. Biol. Chem. 272:27886-27892(1997).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and  
 CC Bcl-x(Beta) isoforms promote apoptosis.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA) ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS  
 CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE  
 CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT  
 CC DETECTABLE LEVEL OF BCL-X(S).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC -----  
 DR EMBL: X82537; CAAS7886.1; -  
 DR EMBL: X82537; CAAS7887.1; -  
 DR EMBL: U10579; AAA19257.1; -  
 DR EMBL: U72350; AAB17353.1; -  
 DR EMBL: U72349; AAB17352.1; -  
 DR EMBL: U34963; AAB7686.1; -  
 DR EMBL: S76513; AAC60701.1; ALT\_INIT.  
 DR EMBL: S78284; AAC60702.1; -  
 DR PDB: 1AF3; 07-JUL-97.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS01260; BH4\_2; 1.  
 DR PROSITE: PS01260; BH4\_3; 1.  
 DR PROSITE: PS01260; BH4\_4; 1.  
 DR PROSITE: PS01260; BH4\_5; 1.  
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 DR PROSITE: PS01260; BH4\_8; 1.  
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 DR PROSITE: PS01260; BH4\_13; 1.  
 DR PROSITE: PS01260; BH4\_14; 1.  
 DR PROSITE: PS01260; BH4\_15; 1.  
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 DR PROSITE: PS01260; BH4\_17; 1.  
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 DR PROSITE: PS01260; BH4\_19; 1.  
 DR PROSITE: PS01260; BH4\_20; 1.  
 DR PROSITE: PS01260; BH4\_21; 1.  
 DR PROSITE: PS01260; BH4\_22; 1.  
 DR PROSITE: PS01260; BH4\_23; 1.  
 DR PROSITE: PS01260; BH4\_24; 1.  
 DR PROSITE: PS01260; BH4\_25; 1.  
 DR PROSITE: PS01260; BH4\_26; 1.  
 DR PROSITE: PS01260; BH4\_27; 1.  
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 DR PROSITE: PS01260; BH4\_39; 1.  
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 DR PROSITE: PS01260; BH4\_41; 1.  
 DR PROSITE: PS01260; BH4\_42; 1.  
 DR PROSITE: PS01260; BH4\_43; 1.  
 DR PROSITE: PS01260; BH4\_44; 1.  
 DR PROSITE: PS01260; BH4\_45; 1.  
 DR PROSITE: PS01260; BH4\_46; 1.  
 DR PROSITE: PS01260; BH4\_47; 1.  
 DR PROSITE: PS01260; BH4\_48; 1.  
 DR PROSITE: PS01260; BH4\_49; 1.  
 DR PROSITE: PS01260; BH4\_50; 1.  
 DR PROSITE: PS01260; BH4\_51; 1.  
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RT Localization of the mouse bcl-x gene.  
 RL J. Immunol. 158:4750-4757(1997).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-x(l) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE AND PERINUCLEAR  
 CC ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).  
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S),  
 CC BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE  
 CC BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-  
 CC TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN  
 CC ACTIVATED.  
 CC -1- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND  
 CC POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN  
 CC POSTNATAL TISSUES.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By  
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
 CC apoptotic activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL: X83574; CAA58557.1; -  
 DR EMBL: L35049; AAS1039.1; -  
 DR EMBL: L35048; AAS1040.1; -  
 DR EMBL: U10102; AAB82174.1; -  
 DR EMBL: U10101; AAB82173.1; -  
 DR EMBL: U10100; AAB82172.1; -  
 DR EMBL: U51279; AAC53460.1; -  
 DR EMBL: U78031; AAB96881.1; -  
 DR EMBL: U78030; AAB96881.1; JOINED.  
 DR HSSP: P53563; IAF3.  
 DR MGD: MGI:88139; Bcl2l.  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004723; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
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 DR PROSITE: PS01260; BH4\_2; 1.  
 DR PROSITE: PS00063; BH4\_2; 1.  
 KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.  
 FT TRASNEM 210 226 POTENTIAL.  
 FT VARSPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 FT VARSPLIC 189 233 DFFVDLYGNNAAESRKGDFRFRNFWLTGTAGVLLGSL  
 FT VARSPLIC 194 233 FSRK -> VRTTPLYCPPLACVSLLEHP (IN ISOFORM  
 FT VARSPLIC 194 233 BCL-X(BETA)).  
 FT VARSPLIC 194 233 LYGNNAAESRKGDFRFRNFWLTGTAGVLLGSLFSR  
 FT VARSPLIC 194 233 -> GHDCGCGSAGITLQSEVTRH (IN ISOFORM BCL-  
 FT VARSPLIC 194 233 X(DELTA-TM)).  
 SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;  
 Query Match 12.0%; Score 105; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0034;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 QY 66 EVCTVLRIGITWGVSLYSVAAGLAVDCVRQAPAMVHALVDCLGFEVRLTATLRR 125  
 DB 125 QVNVNLFPRGVWGVHVAFAFSGALCVESYKENVQLVRSAMATYLNHLEPWIOE 184  
 QY 126 RGGW 129  
 DB 185 NGCW 188  
 RESULT 11  
 BCLX\_PIG STANDARD; PRT; 233 AA.  
 ID BCLX\_PIG  
 AC 077737;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_Taxid=9623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99171363; PubMed=10072723;  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
 RT "Quantification of cardioprotective gene expression in porcine  
 RT short-term hibernating myocardium".  
 RT J. Mol. Cell. Cardiol. 31:147-158(1999).  
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane.  
 CC -1- SUBUNIT: Bcl-x(l) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By  
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
 CC apoptotic activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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CC -----
DR EMBL: AJ001203; CAA04597.1; -
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR pfam: PF00452; Bcl-2; 1.
DR pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis: Mitochondrion; Transmembrane.
KW DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 11.8%; Score 104; DB 1; Length 233;
Best Local Similarity 26.6%; Pred. No. 0 0043;
Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

OY 66 EVCTVILRLGITWGVKVSIVSVAAGLVDCVROAPAMVHALVDCGEFVKTLATWLR 125
Db 125 QVNLLEPRDGVNMGRIYAFPSFGALCVESVDKEMGVLSRIAMWMTYINDHLEPIQE 184
OY 126 RCGW 129
Db 185 NGGM 188

RESULT 12
BCL2_HUMAN
ID BCL2_HUMAN STANDARD: PRT; 233 AA.
AC 007817; 092976;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BCL2L OR BCLX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX MEDLINE=93364977; Pubmed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM BETA).
RA Inohara N., Ohta S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX MEDLINE=95372373; Pubmed=7644501;
RA Sedlak T.W., Oliveira Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Korsmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
RT with Bax.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN [4]

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RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX MEDLINE=96170038; Pubmed=8596636;
RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Korsmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL Nature 379:554-556(1996).
RN [5]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE=97172562; Pubmed=9020082;
RA Sattler M., Liang H., Nettelsheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Fesik S.W.;
RT "Structure of Bcl-XL-Bax peptide complex: recognition between
RT regulators of apoptosis.";
RL Science 275:983-986(1997).
RN [6]
RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RP MEDLINE=96256675; Pubmed=8692274;
RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA Yoon H.S., Nettelsheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA Ng S.L., Fesik S.W.;
RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed
RT cell death.";
RL Nature 381:335-341(1996).
RN [7]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
RX MEDLINE=98118550; Pubmed=9435230;
RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
RA Takahashi A., Kasstan M.B., Griffin D.E., Earnshaw W.C., Velluona M.A.,
RA Hardwick J.M.;
RT "Modulation of cell death by Bcl-XL through caspase interaction.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s)
CC isoform promotes apoptosis.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.
CC Heterodimerization with BAX does not seem to be required for anti-
CC apoptotic activity.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)
CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
CC LYMPHOCTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
CC EMBL: Z23116; CAA80662.1; -
CC DR EMBL: Z23115; CAA80661.1; -
CC DR EMBL: U72396; AAB17354.1; -
CC DR PDB: 1BXI; 29-OCT-97.

```



PDB: 1LXL; 21-APR-97.  
 DR PDB: 1MAZ; 21-APR-97.  
 DR Genew; HGNC:992; BCL2L1.  
 DR MIM; 600039; -.  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH.  
 DR InterPro: IPR004723; Bcl2\_Teg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS0063; BH4-2; 1.  
 DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KM 3D-structure.  
 FT DOMAIN 4 24  
 FT DOMAIN 86 100 BH4.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226  
 FT SITE 61 61  
 FT VARSPLIC 126 188  
 FT VARSPLIC 189 233  
 FT MUTAGEN 61 61  
 FT MUTAGEN 131 133  
 FT MUTAGEN 135 137  
 FT MUTAGEN 138 140  
 FT MUTAGEN 138 138  
 FT MUTAGEN 148 148  
 FT MUTAGEN 156 156  
 FT MUTAGEN 176 176  
 FT MUTAGEN 188 189  
 FT MUTAGEN 189 189  
 FT CONFLICT 70 70  
 FT SEQUENCE 233 AA; 26049 MW; E09D3CDD851AE9BE CRC64;  
 Query Match 11.7%; Score 103; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0054;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

QY 66 ECVTVLLRLGRTGKGVSLYSVAAGLAVDCVROAPAMVHALVDCLGFEVRLTATWLR 125  
 DB 125 QVNNLEFRGVNMGRIYAFVFGALCVESVDKEMQVLVSRIAAWMTATLNLHLEPWIDE 184  
 QY 126 RGGW 129  
 DB 185 NGW 188

RESULT 13  
 BAXB\_HUMAN STANDARD; PRT; 218 AA.  
 AC Q07814;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, cytoplasmic isoform beta.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-B-cell;  
 RX MEDLINE=93364978; PubMed=8358790;  
 RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;  
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
 accelerates programmed cell death."  
 RL Cell 74:609-619(1993).  
 CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
 ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS  
 HOMOLOG FLB 19K PROTEIN.  
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
 FLB 19K PROTEIN, BCL-X(L), MCL-1 AND AL.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
 CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
 ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
 BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
 WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC -1- SIMILARITY: MEMBERS OF THE BCL-2 FAMILY.  
 CC -1- SIMILARITY: CONTRAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTRAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC EMBL: L22474; AAA03620.1; -  
 DR PIR: BA7538; BA7538.  
 DR HSSP; Q07817; 1MAZ.  
 DR Genew; HGNC:959; BAX.  
 DR MIM; 600040; -  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR Apoptosis; Alternative splicing.  
 KM DOMAIN 59 73  
 FT DOMAIN 98 118 BH1.  
 FT DOMAIN 150 165 BH2.  
 FT SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;  
 Query Match 11.5%; Score 101; DB 1; Length 218;  
 Best Local Similarity 22.2%; Pred. No. 0.0078;  
 Matches 34; Conservative 25; Mismatches 52; Indels 42; Gaps 5;

QY 22 PDKELVAQKALGRE-VYHARLRLAGLSWSAPERA-SPAP-GRGLAEVCYLLRLG--- 75  
 DB 13 PTSSQDIKKTGALLDLOGFIQDRAGRG--GEAPDLALDPVPODASTKISGLKRICDEL 70  
 QY 76 -----ITGKVVSLYSVAAGLAVDCVROAP 101  
 DB 71 DSNMELQRMIAVDVDSREVEFRVAADMFSDGNFNMGWVVALFFASKLVLKALCTKVP 130  
 QY 102 AMVHALVDCLGFEVRLTATWLRGGWTDYK 134  
 DB 131 ELIRITMGWTLDFLRRLRLGWTIDOGGWVRLK 163

RESULT 14



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BC1M_MOUSE
ID BCLW_MOUSE STANDARD; PRT; 193 AA.
AC P70345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-w.
GN BCL2L2 OR BCLW.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/10J;
RC MEDLINE=98160183; PubMed=9500547;
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russell L.D., Macgregor G.R.;
RT "Testicular degeneration in Bclw-deficient mice.";
RL Nat. Genet. 18:251-256(1998).
CC -1- FUNCTION: PROMOTES CELL SURVIVAL.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC AND SALIVARY GLAND.
CC -1- DOMAIN: B4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U59746; AAB09056.1; -
DR EMBL: AF030769; AAB86430.1; -
DR HSSP: Q07817; 1MA2.
DR MGD: MGI:108052; Bcl2l2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFS: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis;
KW Apoptosis.
FT DOMAIN 9 29 BH4.
FT DOMAIN 85 104 BH1.
FT DOMAIN 136 151 BH2.
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 11.4%; Score 100; DB 1; Length 193;
Best Local Similarity 24.3%; Pred. No. 0.0086;
Matches 27; Conservative 19; Mismatches 63; Indels 2; Gaps 2;

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QY 22 PTDKEIYVAQAKALGREYVHARLRLAAGLSWAPERASPAFG-GRLAEVCTVLLRLGITWCK 80
DB 37 PAADPLHQAMRAAGDEF-ELRRFRRTSDLAQLAHYTPGSAGQRFYVSDLEPQGGNMR 95
QY 81 VSLSYVAAGLAVDCVRAQAPAMVHALVDCLEFVKRTLATWIRRGWTD 131
DB 96 LVAFVFGAALCAESYKMEKPELVGVQDMMVMVYLETRLADWHTSSGNAE 146

RESULT 15
AR1L_XENLA
ID AR1L_XENLA STANDARD; PRT; 204 AA.
AC Q91828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator R11 (XR11).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Head;
RC MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell survival genes.";
RL Gene 156:171-179(1995).
CC -1- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
DR EMBL: X82461; CAA57844.1; -
DR HSSP: Q07817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2-reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFS: TIGR00865; bcl-2; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis;
KW Apoptosis; Transmembrane.
FT DOMAIN 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSMEM 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;

Query Match 11.3%; Score 99; DB 1; Length 204;
Best Local Similarity 26.6%; Pred. No. 0.011;
Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;
QY 66 EVCTVLLRLGITWCKVSLYSVAAGLAVDCVRAQAPAMVHALVDCLEFVKRTLATWLR 125

```

Db 97 QVMGELFRDGTWGRIVAFSFGALCVESANKENTDLPRIYOMVNTLEHTLOPMAOE 156  
OY 126 RCGW 129  
111  
Db 157 NGW 160

Search completed: April 29, 2003, 11:23:55  
Job time : 6.99217 secs

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GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 10.6527 seconds

(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-4

Perfect score: 878

Sequence: 1 MEVLRRSSVFYFAEIMDAFDR.....TLCSPGFLKAFLLPER 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	134	15.3	236	2	gene bcl-2 protein
2	130	14.8	239	1	transforming prote
3	128.5	14.6	236	2	BCL-2 - rat (fragm
4	128	14.6	236	2	B-cell lymphoma 2
5	127	14.5	236	1	transforming prote
6	125	14.2	205	1	transforming prote
7	124	14.1	199	1	transforming prote
8	118	13.4	216	2	transforming prote
9	114	13.0	227	2	apoptosis regulato
10	113	12.9	233	2	transforming prote
11	106	12.1	233	2	BCL-X protein - ra
12	105.5	12.0	190	2	apoptosis regulato
13	105	12.0	214	2	bcl-x transmembran
14	105	12.0	233	2	bcl-x long - mouse
15	104.5	11.9	232	2	transforming prote
16	103	11.7	233	2	apoptosis regulato
17	101	11.5	218	2	BCL-X protein - rat
18	100	11.2	233	2	Bax-delta protein
19	98	11.2	179	2	BCL-X-long - huma
20	97	11.0	211	2	BCL-2-associated p
21	96	10.9	192	2	BCL-2-associated p
22	94	10.7	133	2	BCL-2-associated p
23	93.5	10.6	143	2	BCL-2-associated p
24	93	10.6	192	2	BCL-2-associated p
25	87	9.9	211	2	hemopoietic-specif
26	83.5	9.5	172	2	probable nitrate/n
27	82.5	9.4	412	2	mannosyltransferas
28	80.5	9.2	860	2	cardamoyl-phosphat
29	80	9.1	1115	2	

30	79	9.0	401	1	A36961	pin biogenesis p
31	78.5	8.9	154	2	I58194	gene bcl-2 protein
32	78.5	8.9	320	2	C72629	hypothetical prote
33	78.5	8.9	419	2	A83133	probable MFS trans
34	78.5	8.9	540	2	T34702	hypothetical prote
35	78	8.9	175	2	I39055	Bcl-2 related - hu
36	78	8.9	212	2	S53257	e antigen precursor
37	77.5	8.8	373	2	H84404	ferrichrome ABC tr
38	77.5	8.8	482	2	C86442	probable amino acil
39	77.5	8.8	822	2	AE2404	DNA helicase (limpo
40	77.5	8.8	1010	2	AH2553	hypothetical prote
41	76.5	8.7	297	2	T46864	nicotinate-nucleot
42	76	8.7	333	2	C95368	hypothetical prote
43	76	8.7	356	2	G81907	probable integral
44	75.5	8.6	495	2	D86442	probable amino acil
45	75.5	8.6	610	2	T09988	probable transcrip

## ALIGNMENTS

RESULT 1  
I53744  
gene bcl-2 protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999  
C:Accession: I53744  
R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.  
Gene 140, 291-292, 1994  
A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.  
A:Reference number: I53744; MUID:94193015; PMID:8144041  
A:Accession: I53744  
A:Status: preliminary; translated from GB/EMBL/DDJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: GB:I14680; MID:9408946; PIDN:AA53662.1; PID:9408947  
A:Genetics:  
A:Gene: bcl-2  
C:Superfamily: bcl transforming protein

Query Match 15.3%; Score 134; DB 2; Length 236;  
Best Local Similarity 20.5%; Pred. No. 7.7e-06;  
Matches 45; Conservative 24; Mismatches 58; Indels 92; Gaps 5;

OY	28	VAQAKALG-----REYVHARLLRAGLSV-----SAPERASBPAG-----	61
DB	1	MAQAGRTGYDNRREIVMKYIHVLSQRCYEMDTGDEDSAPLRAAPTEIFSFQPSNRTPA	60
OY	62	-----	61
DB	61	VHRDTAARTSPRLPLVANNAGPALSPVPVYHLTLRRAGDDFSRRYRDRFAEMSSQLHLTP	120
OY	62	-----GRIAEVCTVLLRLGRTGWKVSLSVAAGLAIDCVQAOAPAMVHALVDCLGEFVRK	117
DB	121	FTARGRAATVVEELFRGVNMGRIIVAFEEFGVGCVSVRREMSPLVDNIALMTETYLNR	180
OY	118	TLATWLRRCGWTVDLKC-VSTDPGFRSHL-VATICS 154	
DB	181	HLHTWIDNGMGDAFVELYGPSPMRPLFDPSWLSLKITLS 219	

RESULT 2  
TVH0A1  
transforming protein bcl-2, splice form alpha - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999  
C:Accession: C37332; A29409; S02452; A24428; A27622; B27622  
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va  
A:Reference number: A37332; MID:92375724; PMID:1508712  
A:Accession: C37332  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation

```

A:Molecule type: DNA
A:Residues: 1-239 <EGU>
A>Note: This report is a correction
R:Tsujimoto, Y.; Croce, C.M.
  Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A:Reference number: A29409; MUID:86259760; PMID:3523487
A:Accession: A29409
A:Molecule type: mRNA
A:Residues: 1-95, 'A', '97-109, 'G', '111-236, 'S', '238-239 <TSD>
A:Cross-references: GB:M33964; MID:g179366; PIDN:AAA51813.1; PID:g179367
A>Note: This sequence has been corrected in reference A37332
R:Seo, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer,
  EMBO J. 7, 123-131, 1988
A:Title: Alternative promoters and exons, somatic mutation and deregulation of the bcl-2
A:Reference number: S02452; MUID:88196071; PMID:2834197
A:Accession: S02452
A:Molecule type: mRNA
A:Residues: 1-239 <SEF>
R:Cleary, M.L.; Smith, S.D.; Sklar, J.
  Cell 47, 19-28, 1986
A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin
A:Reference number: A24428; MUID:87002488; PMID:2875799
A:Accession: A24428
A:Molecule type: mRNA
A:Residues: 1-58, 'T', '60-116, 'R', '118-239 <CLE>
A:Cross-references: GB:M41745; MID:g179370; PIDN:AAA35591.1; PID:g179371
R:Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
  Oncogene Res. 2, 263-275, 1988
A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
A:Reference number: A27622; MUID:88217344; PMID:3285301
A:Accession: A27622
A:Molecule type: mRNA
A:Residues: 1-58, 'T', '60-239 <HUA>
A:Accession: B27622
A:Molecule type: DNA
A:Residues: 1-6, 'S', '8-58, 'T', '60-128, 'C', '130-239 <HUA2>
A>Note: The sequence was determined from the germline gene
C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
C:Genetics:
A:Gene: GDB:BCL2
A:Cross-references: GDB:119031; OMIM:151430
A:Map position: 18q21.3-18q21.3
C:Function:
A:Description: blocks apoptosis in hematopoietic cells
A:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto
Query Match 14.8%; Score 130; DB 1; Length 239;
Best Local Similarity 19.4%; Pred. No. 2e-05;
Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;
OY 37 EYVHARLLRAGLSW-----SAPERASPARC----- 61
DB 17 KYIHKLSQRGYEMDAGDVGAAPGAPAPGIFSSQPGHTRPAPASRDVARTSPLQTPA 76
62 -----GRLAEVCTV 70
DB 77 APGAAGALSPVPVYVHLTLRQAGDDSRKRYRDFALMSQHLNLTPTAGCRATYVEE 136
OY 71 LLRLGITWGVKSVLYSVAAGLAVDCVRQAGPAMVHALVDLCGEFYRKTLATWLRRRGWT 130
DB 137 LFRPGVNMGRIVAAFEFGVCMKVESVNSREMSPLVDNIALMTETYNRLHTWIDONGMD 196
OY 131 DVLCGV-VSTDPGFRSHWL-VATLCS 154
DB 197 AFVELYGPSMRPLDFDSWLSLTKTLLS 222

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C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: 167432
R:Tilly J.L.; Tilly K.I.; Kenton M.L.; Johnson A.L.
Endocrinology 136, 232-241, 1995
A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487; PMID:7828536
A:Accession: 167432
A>Status: Preliminary: translated from GR/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RMS>
A:Cross-references: EMBL:U34964; NID:g1004378; PIDN:AA7687.1; PID:g1004379
C:Superfamily: bcl transforming protein

Query Match      14.6%; Score 128.5; DB 2; Length 236;
Best Local Similarity 18.9%; Pred. No. 2,7e-05;
Matches 44; Conservative 26; Mismatches 62; Indels 101; Gaps 5;

Oy   28 VAQAKALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61
      ||| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
Db   1 MAQAGRTGYDNREIYMKYIHKLSGRGYEMDPDGEDSAPLRRAPPYGIFSPGESNTPPA 60

Oy   62 ----- 61
Db   61 VHRDTAATSPRLPYANAGPALSPVPVHLTLRRAGDDFSRRYRRDFAEKSSQLHTLP 120

Oy   62 ---GRAEVCSTVLRLIGITGWKSILYSVAAGLAVDCCROAPAMAHAYDCIGEYVRK 117
      || | | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
Db   121 FTARGREFATVVEELFRDGVNMGRIVAFEEFGCGVMCVESYNREMYPLVINIMLMETYLNR 180

Oy   118 TLATWTARRGGMTDLKCV-VSTDGFRSHM-----LVATCSFSGFL 159
       || | | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
Db   181 HLHTVIQNNGMDAFVELYGPSMRPLEFDSWSQSLKLTLLSLALVGACITLAGAYL 233


RESULT 4
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7383
R:Tomacic, M.T.; Christmann, M.; Kalina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A>Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A:Reference number: JC7383
A:Contents: Ovary
A:Accession: JC7383
A:Molecule type: mRNA
A:Residues: 1-236 <TOM>
A:Cross-references: GB:AJ271720
C:Comment: This protein has anti-apoptotic function, and supports cell survival.
C:Genetics:
A:Gene: bcl-2
C:Superfamily: bcl transforming protein
C:Keywords: B-cell lymphoma; ovary

Query Match      14.6%; Score 128; DB 2; Length 236;
Best Local Similarity 19.6%; Pred. No. 3.1e-05;
Matches 43; Conservative 26; Mismatches 58; Indels 92; Gaps 5;

Oy   28 VAQAKALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61
      ||| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
Db   1 MAQAGRTGYDNREIYMKYIHKLSGRGYEMDPDVDAFLAAPTPPGIFSPGESNTPPA 60

Oy   62 ----- 61
Db   61 VHRDMAATSPRLPIVATTGPLSPVPVHLTLRRAGDDFSRRYRRDFAEKSSQLHTLP 120

Oy   62 ---GRAEVCSTVLRLIGITGWKSILYSVAAGLAVDCCROAQPMAYHALVDCIGEYVRK 117
      || | | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
Db   121 FTARGREFATVVEELFRDGVNMGRIVAFEEFGCGVMCVESYNREMSFLVINIMLMETYLNR 180

Oy   118 TLATWTARRGGMTDLKCV-VSTDGFRSHM-LVATICS 154

```

Db 181 HLHTWIQDNGMDAFVELYGPVSRPLDFEFSMLSLKTLIS 219

## RESULT 5

TVMSAI

transforming protein bcl-2-alpha - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: A25960; E37332

R:Negrlini, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog

A:Reference number: A90893; PMID:87187643; PMID:3032455

A:Accession: A25960

A:Molecule type: DNA

A:Residues: 1-236 &lt;NEG&gt;

A:Cross-references: GB:L31532; GB:M16506; NID:q468336; PIDN:AAA37282.1; PID:q387109

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A:Reference number: A37332; PMID:92375724; PMID:1508712

A:Accession: E37332

A&gt;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: DNA

A:Residues: 1-33; 'E', '34-220', 'AL', '223-236' &lt;EGU&gt;

C:Genetics:

A:Gene: BCL2

A:Introns: 192/3

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 14.5%; Score 127; DB 1; Length 236;  
Best Local Similarity 19.6%; Pred. No. 3.9e-05;

Matches 43; Conservative 26; Mismatches 58; Indels 92; Gaps 5;

Db 28 VQAQKALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61

1 MAQAGRTGYDNRREIVMKYIHYKLSQRGYEWDADGADADAPGAPPTGIFSFQESNMPA 60

QY 62 ----- 61

Db 61 VHREMAKTSPLRLPVATAGPALSPPVPCVHLTLRRAGDPSRRYRDFAEWSSQLHLTP 120

QY 62 ----GRLAECYTLRLRGITWGVKVSLSYVAAGLAVDCVROAOPAWHNLVDCIGFEFVRK 117

Db 121 FTARGFAIYVEELFRDGVNMGRIVAFEEFGVWCYESVNRKMSPLVDNIALMWTETLNR 180

QY 118 TLATWLRRCGWTDLKCV-VSTDPGFRSHML-VATLCS 154

Db 181 HLHTWIQDNGMDAFVELYGPVSRPLDFEFSMLSLKTLIS 219

RESULT 6

TVHDBI

transforming protein bcl-2; splice form beta - human

N:Alternate names: apoptosis regulator bcl-2

C:Species: Homo sapiens (man)

C&gt;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 15-Oct-1999

C:Accession: B29409; I52566; D37332

R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene

A:Reference number: A29409; PMID:86259760; PMID:3523487

A:Accession: B29409

A:Molecule type: mRNA

A:Residues: 1-205 &lt;TSU&gt;

A:Cross-references: GB:M13995; NID:q179368; PIDN:AAA51814.1; PID:q179369

R:Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.

Blood 79, 229-237, 1992

A:Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-H

A:Reference number: I52566; PMID:92096610; PMID:1339299

A:Accession: I52566

A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-131 <TAN>

A:Cross-references: GB:S72602; NID:q241046; PIDN:AAD14111.1; PID:q4261811

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari

A:Reference number: A37332; PMID:92375724; PMID:1508712

A:Accession: D37332

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 1-33; 'E', '34-95', 'T', '97-109', 'R', '111-205' <EGU>

C:Genetics:

A:Gene: BCL2

A:Cross-references: GDB:119031; OMIM:151430

A:Map position: 18q21.3-18q21.3

C:Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr

Query Match 14.2%; Score 125; DB 1; Length 205;  
Best Local Similarity 17.9%; Pred. No. 5.3e-05;

Matches 32; Conservative 22; Mismatches 39; Indels 86; Gaps 2;

Db 37 EYVHARLLRAGLSW-----SAPERASAPAG----- 61

Db 17 KYTHKLSQRGYEWDADGADADAPGAPPTGIFSFQESNMPA 76

QY 62 ----- 61

Db 77 APGAAGPALSPPVPCVHLTLRRAGDPSRRYRDFAEWSSQLHLTPFTARGFAIYVEE 136

QY 71 LRLRGITWGVKVSLSYVAAGLAVDCVROAOPAWHNLVDCIGFEFVRKTLATWLRRCGW 129

Db 137 LFRDGVNMGRIVAFEEFGVWCYESVNRKMSPLVDNIALMWTETLNLHLHTWIQDNGW 195

RESULT 7

TVMSBI

transforming protein bcl-2-beta - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: B25960

R:Negrlini, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho

A:Reference number: A90893; PMID:87187643; PMID:3032455

A:Accession: B25960

A:Molecule type: DNA

A:Residues: 1-199 &lt;NEG&gt;

A:Cross-references: GB:M16506; NID:q468335; PIDN:AAA37281.1; PID:q387110

C:Genetics:

A:Gene: BCL2

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; transforming protein

Query Match 14.1%; Score 124; DB 1; Length 199;  
Best Local Similarity 19.0%; Pred. No. 6.4e-05;

Matches 38; Conservative 24; Mismatches 46; Indels 92; Gaps 4;

Db 28 VQAQKALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61

Db 1 MAQAGRTGYDNRREIVMKYIHYKLSQRGYEWDADGADADAPGAPPTGIFSFQESNMPA 60

QY 62 ----- 61

Db 61 VHREMAKTSPLRLPVATAGPALSPPVPCVHLTLRRAGDPSRRYRDFAEWSSQLHLTP 120

QY 62 ----GRLAECYTLRLRGITWGVKVSLSYVAAGLAVDCVROAOPAWHNLVDCIGFEFVRK 117

Db 121 FTARGFAIYVEELFRDGVNMGRIVAFEEFGVWCYESVNRKMSPLVDNIALMWTETLNR 180





```

Db      7  RGYDNREIYL-----KYIHYKLSQGYDMAAGEDRPVPAPAPAPAAVAAGASS 59
Oy      61  -----60
Db      60  HHRPSPARLLLVRCPRLLGCAAPGCVHLALROAGDEFSRRYQDPFAQMSGOLHLPFTA 119
Oy      61  GGRLAEVCTVLLRLGITWGVSVLSVAAGLAVDCVROAPAMVHALVDCLGEFVRKTLA 120
Db      120  TGRFVAVVEELFRDGVNMVRIVAFEEFGVMCVESYNREMSPLVDNIATMTTEYLNRHLH 179
Oy      121  TWLRRRGGTDLKCV-VSTDGFRSHW-----LVATLCSGRFL 159
Db      180  NMIDNGGMDAFVELYGNMSMRPLDFDSWISLTKTILSLVLVGACITLGAYL 229

```

Search completed: April 29, 2003, 11:26:35  
 Job time : 12.6527 secs





PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene

PS Claim 2; Page 54-55; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or Bhl3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.

XX Sequence 170 AA;

Query Match 99.2%; Score 871; DB 20; Length 170;  
 Best Local Similarity 99.4%; Pred. No. 7.3e-93;

Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDARDSPDKELVAQAKALGREYVHARLRAGLSWSPERASAP 60  
 DB 1 MEVLRSSVFPAEIMDARDSPDKELVAQAKALGREYVHARLRAGLSWSPERASAP 60  
 OY 61 GGRLAEECTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTIA 120  
 DB 61 GGRLAEECTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTIA 120  
 OY 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAFLLPDER 170  
 DB 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAFLLPDER 170

RESULT 2

ID AAY14156 standard; Protein: 170 AA.

XX AAY14156;

XX 27-JUL-1999 (first entry)

XX Human Bok protein sequence.

XX Bok protein; Bcl-2-related ovarian killer; Bhl3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; human.

XX Homo sapiens.

XX WO9924453-A1.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US23523.

XX 07-NOV-1997; 97US-0064943.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Hsu SY, Hsueh AJW;

DR WPI: 1999-327356/27.  
 DR N-PSDB: AAX61106.

PS Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene

PS Claim 2; Page 57-58; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or Bhl3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.

XX Sequence 170 AA;

Query Match 97.9%; Score 860; DB 20; Length 170;  
 Best Local Similarity 98.2%; Pred. No. 1.4e-91;

Matches 167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDARDSPDKELVAQAKALGREYVHARLRAGLSWSPERASAP 60  
 DB 1 MEVLRSSVFPAEIMDARDSPDKELVAQAKALGREYVHARLRAGLSWSPERASAP 60  
 OY 61 GGRLAEECTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTIA 120  
 DB 61 GGRLAEECTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTIA 120  
 OY 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAFLLPDER 170  
 DB 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAFLLPDER 170

RESULT 3

ID AAY14153 standard; Protein: 213 AA.

XX AAY14153;

XX 27-JUL-1999 (first entry)

XX Rat Bok protein sequence.

XX Bok protein; Bcl-2-related ovarian killer; Bhl3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; rat.

XX Rattus rattus.

XX WO9924453-A1.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US23523.

XX 07-NOV-1997; 97US-0064943.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Hsu SY, Hsueh AJW;  
 XX  
 PI  
 DR WPI: 1999-327356/27.  
 DR N-PSDB; AAX61103.  
 XX  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 XX  
 PS Claim 2: Page 53-54; 62pp; English.  
 XX  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 XX Sequence 213 AA:  
 SQ  
 Query Match 96.4%; Score 846.5; DB 20; Length 213;  
 Best Local Similarity 79.8%; Pred. No. 6.9e-90;  
 Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;  
 QY 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYHARLLRAGLSNAPERASPAP 60  
 DB 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYHARLLRAGLSNAPERASPAP 60  
 QY 61 GGRLAECVTLRL-----GTT 77  
 DB 61 GGRLAECVTLRLGDELEQIRPSVYRNVARQLHIPLOSEPVTDAFLAVAGHIFSAGIT 120  
 QY 78 WCKVSVLSYAAGLAVDCVROAPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCVY 137  
 DB 121 WCKVSVLSYAAGLAVDCVROAPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCVY 180  
 QY 138 STDGFRSHWLVAATLCSFGRLKAFFLLPER 170  
 DB 181 STDGFRSHWLVAATLCSFGRLKAFFLLPER 213  
 Db  
 RESULT 4  
 ID AAY14155 standard; Protein; 213 AA.  
 XX AAY14155;  
 AC  
 XX 27-JUL-1999 (first entry)  
 DT  
 XX Human Bok protein sequence.  
 DE  
 XX Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX W0924453-A1.  
 PN  
 XX

PD 20-MAY-1999.  
 XX  
 XX  
 PF 04-NOV-1998; 98WO-US23523.  
 XX  
 XX 07-NOV-1997; 97US-0064943.  
 XX  
 PR  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 XX  
 PI Hsu SY, Hsueh AJW;  
 XX  
 DR WPI: 1999-327356/27.  
 DR N-PSDB; AAX61105.  
 XX  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 XX  
 PS Claim 2: Page 55-56; 62pp; English.  
 XX  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 XX Sequence 213 AA:  
 SQ  
 Query Match 94.4%; Score 828.5; DB 20; Length 213;  
 Best Local Similarity 78.4%; Pred. No. 8.5e-88;  
 Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;  
 QY 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYHARLLRAGLSNAPERASPAP 60  
 DB 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYHARLLRAGLSNAPERASPAP 60  
 QY 61 GGRLAECVTLRL-----GTT 77  
 DB 61 GGRLAECVTLRLGDELEQIRPSVYRNVARQLHIPLOSEPVTDAFLAVAGHIFSAGIT 120  
 QY 78 WCKVSVLSYAAGLAVDCVROAPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCVY 137  
 DB 121 WCKVSVLSYAAGLAVDCVROAPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCVY 180  
 QY 138 STDGFRSHWLVAATLCSFGRLKAFFLLPER 170  
 DB 181 STDGFRSHWLVAATLCSFGRLKAFFLLPER 213  
 Db  
 RESULT 5  
 ID AAB41444 standard; Protein; 213 AA.  
 XX AAB41444;  
 AC  
 XX 08-FEB-2001 (first entry)  
 DT  
 XX Human ORFX ORF1208 polypeptide sequence SEQ ID NO:2416.  
 DE  
 XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnerability; antiproliferative; antiparkinsonian; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;

KM		immunostimulant; thrombolytic; coagulant; vasotropic; antiplatelet;
KV		hypertensive; dermatological; immunosuppressive; antinflammatory;
KW		antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KX		antineuragic; gene therapy; cancer; proliferative disorder; hypertension;
KY		neurodegenerative disorder; osteoarthritis; graft vs host disease;
KZ		cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KA		cholesterol ester storage; systemic lupus erythematosus; infection;
KB		severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KC		allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KD		bone damage; cartilage damage; antinflammatory disease; coagulation;
KE		thrombosis; contraceptive.
KF		
KG	Homo sapiens.	
KH		
KI	WO200058473-A2.	
KJ		
KK	05-OCT-2000.	
KL		
KM	31-MAR-2000; 2000MO-US08621.	
KN		
KO	31-MAR-1999; 99US-0127607.	
KP	02-APR-1999; 99US-0127636.	
KQ	05-APR-1999; 99US-0127728.	
KR	30-MAR-2000; 2000US-0540763.	
KS		
KT	(CDRA-) CUBAGEN CORP.	
KU		
KV	Shinkets RA, Leach M;	
KW		
KX	WPI: 2000-602362/57.	
KY	N-PSDB; AAC75653.	
KA		
KB		
KC	Novel nucleic acids and peptides derived from open reading frame X,	
KD	useful for treating e.g. cancers, proliferative disorders,	
KE	neurodegenerative disorders and cardiovascular disease -	
KF		
KG	Claim 11; Page 1750-1751; 5507pp; English.	
KH		
KI	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,	
KJ	which represent the human ORFX open reading frames 1 to 3161. The ORFX	
KK	sequences have activities such as: cytostatic; hepatotropic; vulnerrary;	
KL	antisporitic; antiparkinsonian; nootropic; neuroprotective;	
KM	osteopethic; anticovulsant; antiarthritic; immunosuppressant;	
KN	immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;	
KO	antidiabetic; hypotensive; dermatologicl; immunosuppressive;	
KP	antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;	
KQ	antithyroid; and antinaeemic. The sequences can be used for determining	
KR	the presence of or predisposition to, or preventing or treating	
KS	pathological conditions associated with an ORFX-associated disorder. The	
KT	nucleic acids can be used to express ORFX proteins in gene therapy	
KU	vectors. The proteins and nucleic acids may be used to treat cancers,	
KV	proliferative disorders, neurodegenerative disorders, osteoarthritis,	
KW	graft vs host disease, cardiovascular disease, diabetes mellitus,	
KX	hyperextension, hypothyroidism, cholesterol ester storage, systemic lupus	
KY	erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,	
KZ	bacterial or fungal infection, malaria, autoimmune disorders, asthma,	
KA	allergic, aplastic anaemia, burns, wounds, bone and cartilage damage,	
KB	nocturnal haemoglobinuria, antinflammatory disease; to enhance	
KC	coagulation; to inhibit thrombosis; and as a contraceptive.	
KD		
KE		
KF	Sequence 213 AA:	
KG		
KH	Query Match 93.1%; Score 817.5; DB 21; Length 213;	
KI	Best Local Similarity 77.0%; Pred. No. 1.6e-86;	
KJ	Matches 164; Conservative 2; Mismatches 4; Indels 43; Gaps 1	
KK		
KL	1 MEVLRSSVFAAEINDAFDSPTDELYAQAALGREYVHARLLRAGLSWSAPERASPAP 60	
KM		
KN	1 MEVLRSSVFAAEINDAFDRMPETDELVAQAALGREYHARLLRAGLSMSAPERASPAP 60	
KO		
KP	61 GGRLAEVCYTVLRL-----GTT 77	
KQ		
KR	61 GGRLAEVCATLLRLDDELEMRPSYRNVARQLHTSLQSEPVYTDAFLAVAGHIIFSAGTT 120	

QY	78	WCKVSVLSVVAAGLAVDCVROAQPMAVHALVDCGEEFPRKLTATWLRBGGTDLKCV	137
Db	121	WKKVSVLSVVAAGLAVDCVROAQPMAVHALVDCGEEFPRKLTATWLRBGGTDLKCV	180
QY	138	STDGFSRSHMLVATLCGFSGRFLKAAFFLLDPER	170
Db	181	STDGFSRSHMLVATLCGFSGRFLKAAFFLLDPER	213
RESULT	6		
ID	AAB85665	standard; Protein: 134 AA.	
XX	AAB85665;		
XX	29-OCT-2001	(first entry)	
DE	Human Bcl-2-like polypeptide (clone HHEH17).		
KW	Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;		
KM	respiratory; cardiovascular; antirhectic; immunostimulant; vaccine;		
OS	immunosuppressive; antiinflammatory; gene therapy.		
XX	Homo sapiens.		
XX	WO200157060-A1.		
XX	09-AUG-2001.		
XX	31-JAN-2001; 2001WO-US03080.		
XX	01-FEB-2000; 2000US-0179487.		
XX	07-FEB-2000; 2000US-0180697.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
PI	Ruben SM, Duan DR, Ni J;		
DR	WPI; 2001-476279/51.		
XX	N-PSDB; AAH47021.		
XX	Nucleic acids encoding human Bcl-2-like polypeptides, useful for		
XX	preventing, diagnosing and/or treating -		
XX	Claim 12; Page 277-278; 2855pp; English.		
XX	The invention provides nucleic acid molecules (NAM1) encoding 4 human		
XX	Bcl-2-like polypeptides (PEP1). The NAM1 and PEP1 may be used in the		
XX	prevention, diagnosis and treatment of diseases associated with		
XX	inappropriate Bcl-2-like polypeptides' expression. The NAM1 may be used		
XX	to produce the soluble Bcl-2-like polypeptides by standard recombinant		
XX	methodology. The polypeptides may also be used as antigens in the		
XX	production of antibodies against Bcl-2 and in assays to identify		
XX	modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies		
XX	and antagonists may be used to down regulate expression and activity.		
XX	The anti-PEP1 antibodies may also be used as diagnostic agents for		
XX	detecting the presence of Bcl-2 polyps in samples (e.g. by enzyme linked		
XX	immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed		
XX	and/or treated by the above methods include: immunodeficiencies (e.g.		
XX	a gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune		
XX	disorders (e.g. Rheumatoid arthritis and Grave's disease), allergic		
XX	reactions, inflammations, respiratory diseases and cardiovascular		
XX	disorders (a full list of disorders is given in the specification). The		
XX	present sequence represents a human Bcl-2-like polypeptide.		
SO	Sequence	134 AA;	
Query Match	56.4%;	Score 495; DB 22; Length 134;	
Best Local Similarity	75.4%;	Pred. No. 2.4e-49;	
Matches	98; Conservative	5; Mismatches 21; Indels 6; Gaps 1;	
QY	41	ATLRAGLSWSAPERASAPGGRLAEVCTVLLRLGITWGVSVLSVVAAGLAVDCVROAQ	100

Db 11 AROHLSTL-----QSEPVVTDALFLAVAGHIFSAGITWGKVVSLVVAAGLADVCRQAQ 64  
 QY 101 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 160  
 Db 65 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 124  
 QY 161 AAFELLPPER 170  
 Db 125 AAFVLLPPER 134

RESULT 7  
 AAB58949  
 ID AAB58949 standard; Protein; 176 AA.  
 AC AAB58949;  
 DT 27-MAR-2001 (first entry)  
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.  
 XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KM neutropenic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 KM antidiabetic; antiinflammatory; antilucer; vulnerary; anticonvulsant;  
 KM antibacterial; antifungal; antiparasitic; cardiant; immune disorder;  
 KM Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KM autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KM cardiovascular disorder; wound healing; neurological disease.  
 XX Homo sapiens.  
 OS WO20055173-A1.  
 PN 21-SEP-2000.  
 XX 08-MAR-2000; 2000WO-US05881.  
 XX 12-MAR-1999; 99US-0124270.  
 PR (HUMA-) HUMAN, GENOME SCI INC.  
 PA Rosen CA, Ruben SM;  
 PI MPI: 2000-611515/58.  
 DR N-PSDB: AAF21852.  
 XX New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention,  
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular  
 PT disorders and neurological diseases -  
 XX Claim 11; Page 1103; 1299pp; English.  
 PS Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
 CC isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
 CC neutropenic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 CC antidiabetic; antiinflammatory; antilucer; vulnerary; anticonvulsant;  
 CC antibacterial; antifungal; antiparasitic and cardiant activity. The  
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
 CC particularly breast and ovarian cancer. The nucleic acid sequences,  
 CC proteins, agonists and antagonists may also be used in the diagnosis,  
 CC prevention and treatment of immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; cardiovascular disorders such as  
 CC myocardial ischaemias; wound healing; neurological diseases such as

CC cerebral anoxia and epilepsy; and infectious diseases.  
 XX SQ Sequence 176 AA:  
 Query Match 56.4%; Score 495; DB 21; Length 176;  
 Best Local Similarity 75.4%; Pred. No. 3.4e-49;  
 Matches 98; Conservative 5; Mismatches 21; Indels 6; Gaps 1;

QY 41 ARLLRAGLSMSAPERSPAAGRLAFCVTLRLGLTWKGVSLSVAGLADVCRQAQ 100  
 Db 53 AROHLSTL-----QSEPVVTDALFLAVAGHIFSAGITWGKVVSLVVAAGLADVCRQAQ 106  
 QY 101 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 160  
 Db 107 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 166  
 QY 161 AAFELLPPER 170  
 Db 167 AAFVLLPPER 176

RESULT 8  
 ABB63760  
 ID ABB63760 standard; Protein; 247 AA.  
 AC ABB63760;  
 DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster polypeptide SEQ ID NO 18072.  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.  
 KM Drosophila melanogaster.  
 OS WO200171042-A2.  
 PN 27-SEP-2001.  
 XX 23-MAR-2001; 2001WO-US09231.  
 XX 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 PA (PEKE ) PE CORP NY.  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 DR MPI: 2001-656860/75.  
 DR N-PSDB: ABL07863.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX Disclosure: SEQ ID NO 18072; 21pp + Sequence Listing; English.  
 PS The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (AAB57737-ABR72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 247 AA:  
 Query Match 19.8%; Score 173.5; DB 22; Length 247;

Best Local Similarity 27.8%, Pred. No. 1.1e-11;  
Matches 44; Conservative 20; Mismatches 41; Indels 53; Gaps 4;

OY 25 KELVAQAKALGREYHARLLRAGL-----SWGAP----- 53  
DB 87 ODIIOGRCICGCHYIKRRRLRSGLFNKKLIGLORISILGSTMGVIRDVFPVAVVLGDEL 146  
OY 54 ERASPA-----PGR-----LAECYVLLRLGTTGKVSLSVAGL 91  
DB 147 ERMHPIRYNGVAKQICRNPGGEFHTPDVSLLGAVGRELFVEVETWSKVISLFAIAGL 206  
OY 92 AVDCVROAPAMVHALVDCIGEFVRKTLATWLRRRGW 129  
DB 207 SVDVCRQGHPEYLPKIMESVEVIEDLVPMINENGW 244

RESULT 9  
ABB64401  
ID ABB64401 standard; Protein: 846 AA.  
XX  
AC ABB64401;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 19995.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
XX  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI: 2001-6556860/75.  
XX  
DR N-PSDB: ABL08504.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Disclosure: SEQ ID NO 19995; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 846 AA;

Query Match 19.7%; Score 173; DB 22; Length 846;  
Best Local Similarity 28.2%; Pred. No. 6.3e-11;  
Matches 44; Conservative 17; Mismatches 43; Indels 52; Gaps 3;

OY 26 ELVNOAKALGREYHARLLRAG-LSWSAPER----- 55  
::: | | | : | | | | | | : |

DB 96 DIINOQKICGQYIARLRACVILNRKYTORLNIIDPGSSHVVEVPALNSGEELE 155  
OY 56 -----ASPAQGRILAE-----VCTVLLRLGTTGKVSLSVAGLAV 93  
DB 156 MHPRYTINSRQLSRAPGGELESDMAPMLNLVAKDLFRSSITGKIIISFAVGGFAI 215  
OY 94 DCVROAPAMVHALVDCIGEFVRKTLATWLRRRGW 129  
DB 216 DCVROGHFDYLOCLIDGLAEITLEDLVYVLLDNGW 251

RESULT 10  
AAW02383  
ID AAW02383 standard; Protein: 239 AA.  
XX  
AC AAW02383;  
XX  
DT 04-JUN-1997 (first entry)  
XX  
DE Human BCL2.  
XX  
KW Sense oriented; genetic suppressor element; GSE; reverse;  
KW BCL2; gene; mediated; suppression; apoptosis; mammalian; cell;  
KW inhibition; sensitisation; cancer; chemotherapeutic agent;  
KW increase; treatment; induction; virus; infection; death;  
KW disease; haematopoietic; neurological; recombinant construct;  
KW decrease; expression; anticancer; non-Hodgkin's lymphoma;  
KW B cell malignancy.  
XX  
OS Homo sapiens.  
XX  
PN WO9629403-A1.  
XX  
PD 26-SEP-1996.  
XX  
PF 14-MAR-1996; 96WO-US03545.  
XX  
PR 17-MAR-1995; 95US-0405702.  
XX  
PA (UNITI ) UNIV ILLINOIS FOUNO.  
XX  
PI Holzmayer TA, Roninson IB, Schott B, Tarasiewicz DG;  
XX  
DR WPI: 1996-443179/44.  
XX  
DR N-PSDB: AAT33694.  
XX  
PT Sense oriented genetic suppressor element - for reversing BCL2  
PT mediated inhibition of apoptosis, and for sensitising cancer cells  
PT against chemotherapeutic agents  
XX  
PS Claim 20; Pages 37-38; 66pp; English.  
XX  
CC The present sequence is human BCL2 from which a peptide  
CC capable of inhibiting BCL2 gene, or gene product, function in a  
CC cell can be derived. The cDNA sequence encoding the peptide is a  
CC sense oriented genetic suppressor element (GSE) for reversing  
CC BCL2 mediated suppression of apoptosis in a mammalian cell. The  
CC GSE and its peptide product can be used to sensitize cancer cells  
CC to chemotherapeutic agents, and to increase apoptosis, especially  
CC for the treatment of cancer, but more generally to induce virus  
CC infected cell death, or to treat apoptosis related diseases of  
CC haematopoietic or neurological cells. The GSE peptide product or a  
CC recombinant construct encoding the GSE can be used to decrease  
CC BCL2 gene expression by exerting an anticancer effect, e.g. in  
CC cases of non-Hodgkin's lymphoma and B cell malignancy.  
XX  
SQ Sequence 239 AA;

Query Match 14.9%; Score 131; DB 17; Length 239;  
Best Local Similarity 19.4%; Pred. No. 9e-07;  
Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;

OY 37 EYVHARLLRAGLSW-----SAPERASPARC----- 61  
::: | | | : | | | | | | : |

```

Db      17 KTIHYLSQRYGEMDAGVGAAPGGAAPAGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76
OY      62 -----GRLAEVCTV 70
Db      77 APCAAGPALSPVPVPHALRQAGDPSRRYRGDAEMSSOLHLPPTARGRFATVVEE 136
OY      71 LRLGITMGKVVSLYSVAGLAVDCVROQAPAMVHALVDCLEGFVRKTLATWLRRGWMT 130
Db      137 LFRDGVNMGRIYAFFEFGVMSVESVNRKMSPLVDNIALMTEYLNRHLHTWIDNGMD 196
OY      131 DVLKCV-VSTDGFRSHWL-VATLCS 154
Db      197 AFVELYGPSMRPLDFDSWLSLTKTLIS 222

```

## RESULT 11

AAG64036  
ID AAG64036 standard; protein; 239 AA.

AC AAG64036;

DT 10-SEP-2001 (first entry)

DE Human Bcl-2 protein mutant #1.

Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.

OS Homo sapiens.

OS Synthetic.

PN WO200142459-A1.

PD 14-JUN-2001.

PF 07-DEC-2000; 2000WO-JP08667.

PR 09-DEC-1999; 99JP-0350427.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Shibazaki F, Kuma H;

DR WPI; 2001-381681/40.

PT New apoptosis inhibitors, useful for treating apoptosis related disorders

PS Claim 5; Page 30-31; 43pp; Japanese.

CC The invention relates to an apoptosis inhibitor comprising the amino acid sequence of Bcl-2 protein in which at least one serine residue is substituted by alanine or aspartic acid. The protein has increased apoptosis inhibitory activity compared with the wild type Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present sequence is a mutant Bcl-2 protein of the invention.

SQ Sequence 239 AA;

Query Match 14.9%; Score 131; DB 22; Length 239;

Best Local Similarity 19.4%; Pred. No. 9e-07; Mismatches 53; Indels 88; Gaps 4;

Db 37 EYVHARLLRAGLSM-----SAPERASAPAG----- 61

Db 17 KTIHYLAQRYGEMDAGVGAAPGGAAPAGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76

OY 62 -----GRLAEVCTV 70

Db 77 APCAAGPALSPVPVPHALRQAGDPSRRYRGDAEMSSOLHLPPTARGRFATVVEE 136

OY 71 LRLGITMGKVVSLYSVAGLAVDCVROQAPAMVHALVDCLEGFVRKTLATWLRRGWMT 130

```

Db      137 LFRDGVNMGRIYAFFEFGVMSVESVNRKMSPLVDNIALMTEYLNRHLHTWIDNGMD 196
OY      131 DVLKCV-VSTDGFRSHWL-VATLCS 154
Db      197 AFVELYGPSMRPLDFDSWLSLTKTLIS 222

```

## RESULT 12

AAG64038  
ID AAG64038 standard; protein; 239 AA.

AC AAG64038;

DT 10-SEP-2001 (first entry)

DE Human Bcl-2 protein mutant #3.

Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.

OS Homo sapiens.

OS Synthetic.

PN WO200142459-A1.

PD 14-JUN-2001.

PF 07-DEC-2000; 2000WO-JP08667.

PR 09-DEC-1999; 99JP-0350427.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Shibazaki F, Kuma H;

DR WPI; 2001-381681/40.

PT New apoptosis inhibitors, useful for treating apoptosis related disorders

PS Claim 7; Page 33-34; 43pp; Japanese.

CC The invention relates to an apoptosis inhibitor comprising the amino acid sequence of Bcl-2 protein in which at least one serine residue is substituted by alanine or aspartic acid. The protein has increased apoptosis inhibitory activity compared with the wild type Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present sequence is a mutant Bcl-2 protein of the invention.

SQ Sequence 239 AA;

Query Match 14.9%; Score 131; DB 22; Length 239;

Best Local Similarity 19.4%; Pred. No. 9e-07; Mismatches 53; Indels 88; Gaps 4;

Db 37 EYVHARLLRAGLSM-----SAPERASAPAG----- 61

Db 17 KTIHYLSQRYGEMDAGVGAAPGGAAPAGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76

OY 62 -----GRLAEVCTV 70

Db 77 APCAAGPALSPVPVPHALRQAGDPSRRYRGDAEMSSOLHLPPTARGRFATVVEE 136

OY 71 LRLGITMGKVVSLYSVAGLAVDCVROQAPAMVHALVDCLEGFVRKTLATWLRRGWMT 130

Db 137 LFRDGVNMGRIYAFFEFGVMSVESVNRKMSPLVDNIALMTEYLNRHLHTWIDNGMD 196

OY 131 DVLKCV-VSTDGFRSHWL-VATLCS 154

Db 197 AFVELYGPSMRPLDFDSWLSLTKTLIS 222

RESULT 13  
 ID AAF80987 standard; protein; 239 AA.  
 AC AAF80987;  
 DT 17-DEC-1990 (first entry)  
 DE Sequence of bcl-2-alpha encoded by sequence of bcl-2 cDNA corresp. to the 5.5 kb transcript.  
 KW B-cell neoplasm; diagnosis; follicular lymphomas.  
 OS Homo sapiens.  
 PN EP252685-A.  
 PD 13-JAN-1988.  
 PF 02-JUL-1987; 87EP-0305863.  
 PR 09-JUL-1986; 86US-0883687.  
 PA (WIST-) WISTAR CORP.  
 PI Tsujimoto Y, Croce CM;  
 DR WPI: 1988-008633/02.  
 DR N-PSDB: AAN81292.  
 XX  
 PT Detection of B-cell neoplasms -  
 PT by extr. of proteins or RNA from B-cells and quantitation using  
 PT specific antibody or DNA probe  
 PS  
 XX  
 PS Claim 12; Fig 2A-2D; 23pp; English.  
 CC A human bcl-2 gene substantially free of introns is claimed. Also  
 CC claimed is a substantially pure preparation of a protein having an  
 CC N-terminal end encoded by the first exon of the human bcl-2 gene wherein  
 CC said protein is bcl-2-alpha having about 239 (AAF80987) or 205 (AAF80988)  
 CC AA residues. B-cell neoplasms which are associated with t(14;18)  
 CC chromosome translocations cause an increase in expression of both the  
 CC mRNA and the protein products of the bcl-2 gene. This is used to detect  
 CC B-cell neoplasms including follicular lymphomas as well as other  
 CC lymphomas. Bacterial isolates available as ATCC 67147 and 67148 can be  
 CC used to express bcl-2 gene products alpha (AAN81292) and beta (AAN81293)  
 CC resp. in bacteria.  
 XX  
 SO Sequence 239 AA;  
 Query Match 14.8%; Score 130; DB 9; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 1.2e-06;  
 Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;  
 OY 37 EYVHARLRAGLSW-----SAPERASAPG----- 61  
 DB 17 KYIHVLSQRGYEMDAGVGAAPGAPGIFSSQPGHTPHPAASRDPVARTSPLQTPA 76  
 OY 62 -----GRLAEVCTV 70  
 DB 77 AFGAAGALSPVPVPHALRQAGDDFSRRYRGDFAEMSSQLHTPTTARGRFATVVEE 136  
 OY 71 LRLIGITMGKVSLSYVAGIACVDCVROAQPAMVHALVDCIGEFVRKTLATWLRRRGWT 130  
 DB 137 LFRDGVNMGRIYAFEEFGVCMCVESVNREMSPLVDNIALMWTETYNRLHTWIDQNGMD 196  
 OY 131 DVLKCV-VSTDPGFRSHL-VATLCS 154  
 DB 197 AFVELYGPSMRPLFDFSWLSIKTLIS 222

RESULT 14  
 AAR42312

ID AAR42312 standard; Protein; 239 AA.  
 AC AAR42312;  
 DT 03-MAY-1994 (first entry)  
 DE Bcl-2 oncogene product.  
 KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene; expression; myc.  
 OS Homo sapiens.  
 PN W09320200-A.  
 PD 14-OCT-1993.  
 PF 02-APR-1993; 93WO-GB00686.  
 PR 02-APR-1992; 92GB-0007275.  
 PR 02-APR-1992; 92GB-0007276.  
 PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 PI Evan GI;  
 DR WPI: 1993-336908/42.  
 DR N-PSDB: AAO49815.  
 XX  
 PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -  
 PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with  
 PT antisense oligo:nucleotide(s), also increasing survival of  
 PT cultured cells by expressing BCL-2  
 PS  
 XX  
 PS Disclosure: Page 76-77; 109pp; English.  
 CC A DNA construct comprising the bcl-2 coding sequence under control  
 CC of elements allowing its expression is claimed. Myc-induced cell  
 CC death can be inhibited in cultured cells by expressing bcl-2.  
 CC Myc-induced cell death can be de-inhibited in tumour cells by admin.  
 CC of bcl-2 antisense oligonucleotides.  
 XX  
 SO Sequence 239 AA;  
 Query Match 14.8%; Score 130; DB 14; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 1.2e-06;  
 Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;  
 OY 37 EYVHARLRAGLSW-----SAPERASAPG----- 61  
 DB 17 KYIHVLSQRGYEMDAGVGAAPGAPGIFSSQPGHTPHPAASRDPVARTSPLQTPA 76  
 OY 62 -----GRLAEVCTV 70  
 DB 77 AFGAAGALSPVPVPHALRQAGDDFSRRYRGDFAEMSSQLHTPTTARGRFATVVEE 136  
 OY 71 LRLIGITMGKVSLSYVAGIACVDCVROAQPAMVHALVDCIGEFVRKTLATWLRRRGWT 130  
 DB 137 LFRDGVNMGRIYAFEEFGVCMCVESVNREMSPLVDNIALMWTETYNRLHTWIDQNGMD 196  
 OY 131 DVLKCV-VSTDPGFRSHL-VATLCS 154  
 DB 197 AFVELYGPSMRPLFDFSWLSIKTLIS 222

RESULT 15

AAR70331

ID AAR70331 standard; Protein; 239 AA.

AC AAR70331;

DT 27-SEP-1995 (first entry)



DE Human bcl-2 protein.  
 XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
 KM chemoresistance.  
 XX

OS Homo sapiens.

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI; 1995-139394/18.

XX Antl-code oligomers which bind to bcl-2 mRNA - for the treatment  
 PT of human solid tumours, esp. breast cancer  
 XX

PS Disclosure; Page 71-72; 108pp; English.

XX The human bcl-2 gene encodes a 25 kDa protein (AAR70331). Antisense  
 CC oligonucleotides have been designed to bind sites in mRNA transcribed  
 CC from the bcl-2 gene, thereby reducing expression of the bcl-2 protein  
 CC and inducing cell death in certain cancer cells.

XX Sequence 239 AA;

Query Match 14.8%; Score 130; DB 16; Length 239;

Best Local Similarity 19.4%; Pred. No. 1.2e-06;  
 Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;

OY 37 EYVHARLLRAGLSW-----SAPERASPAAG----- 61

DB 17 KYTHYKLSQRGYWDAGDVGAPGAAPAGGIRSSQPGHTPHPAASRDVPARTSPLOTPA 76

OY 62 -----GRLAEYCTV 70

DB 77 APGAAGPALSPVPVPHLALRQAGDPSRRYRGDEPAEMSSQLHLTPFTARGRFATVEE 136

OY 71 LRLGITWGKVSLSYSAAGLAVDCYRQAPAWVHALVDCLGFEVRRKTLATWLRRGWT 130

DB 137 LFRDGVNMGRIYAFEEGGVMCVESVNRKMSPLVDNIALMTEYLNRHLHTWTIQDNGWD 196

OY 131 DVLKCV-VSTDPGFRSHWL-VATLCS 154

DB 197 AFVELYGPMSWRLPFDPSWLSLKTLLS 222

Search completed: April 29, 2003, 11:23:22  
 Job time : 26.9661 secs





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DB 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
OY 181 STKPGFRSHMLVATLCSFGRLKAAFFLLP 213
DB 181 STKPGFRSHMLVATLCSFGRLKAAFFLLP 213

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## RESULT 2

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035425 PRELIMINARY; PRT: 213 AA.

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ID 035425
AC 035425.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BCL-2-related ovarian killer protein.
GN BOK OR BOKL OR BOK OR MTD.
OS Rattus norvegicus (Rat), and
OS Mus musculus (Mouse), Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116, 10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;
RX MEDLINE=98024143; Pubmed=9356461;
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;
RT "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in
RT reproductive tissues and heterodimerizes with selective anti-apoptotic
RT Bcl-2 family members."
RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;
RX Hsu S.Y., Hsueh A.J.W.;
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Inohara N., Ekheraie D., Garcia I., Carrilo R., Merino J., Merry A.,
RA Chen S., Nunez G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RX EMBL: AF027954; AAB87418.1; -
DR EMBL: AF027707; AAC53582.1; -
DR MGI: 1858494; BOK.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SO SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

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Query Match 97.8%; Score 1076; DB 11; Length 213;
Best Local Similarity 98.6%; Pred. No. 9.1e-87;
Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
DB 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
OY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 120
OY 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
DB 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
OY 181 STKPGFRSHMLVATLCSFGRLKAAFFLLP 213
DB 181 STKPGFRSHMLVATLCSFGRLKAAFFLLP 213

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## RESULT 3

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09UMX3 PRELIMINARY; PRT: 212 AA.

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ID 09UMX3
AC 09UMX3.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BCL-2-related ovarian killer protein (Similar to BCL-2-related ovarian
DE killer protein-like-PENDING) (BCL-2-related ovarian killer
DE protein-like).
GN BOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H.;
RT "Gene expression of a human homolog of BCL-2-related ovarian killer
RT protein."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RA Strausberg R.;
RX Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RA Strausberg R.;
RX Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF174487; AAD51719.1; -
DR EMBL: BC006203; AAH06203.1; -
DR EMBL: BC017214; AAH17214.1; -
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SO SEQUENCE 212 AA; 23280 MW; 053ED605FF8EF5B2 CRC64;

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Query Match 92.5%; Score 1017.5; DB 4; Length 212;
Best Local Similarity 93.9%; Pred. No. 1.2e-81;
Matches 200; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

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OY 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
DB 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
OY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 119
OY 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
DB 120 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 179
OY 181 STKPGFRSHMLVATLCSFGRLKAAFFLLP 213
DB 180 STKPGFRSHMLVATLCSFGRLKAAFFLLP 212

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## RESULT 4

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091812 PRELIMINARY; PRT: 213 AA.

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ID 091812
AC 091812.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-2-related ovarian killer protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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OC Gallus.
  NCBI_TaxID=9031;
  [1]
  RP SEQUENCE FROM N.A.
  MEDLINE=20487164; PubMed=11034351;
  RA Zhang H., Holzgrevé W., de Geyter C.;
  RT "Evolutionarily conserved Bcl proteins in the Bcl-2 family.";
  RL FEBS Lett. 480:311-313(2000).
  DR EMBL: AF275944; AAF81282.1;
  DR InterPro: IPR000712; Bcl2_BH.
  DR InterPro: IPR002475; BCL2_family.
  DR Pfam: PF00452; Bcl-2; 1.
  DR SMART: SM00337; BCL; 1.
  DR PROSITE: PS50062; BCL2_FAMILY; 1.
  SO SEQUENCE 213 AA; 23619 MW; B3AF7049F25442E3 CRC64;

Query Match
  Best Local Similarity 79.5%; Score 874; DB 13; Length 213;
  Matches 164; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAALGREYVHARLLRAGLSMSAPERASAP 60
DB 1 MEVLRRSSVFAAEVMEFDRSPDKELVSOAKALCRDIYNSRLIRAGVSMKPEHNPVP 60
OY 61 GGRLAECVTLRLGDELLEQIRSVYRNVARQLHIPLQSEPVYTDALAVAGHIFSAGIT 120
DB 61 GGRLAECVTLRLGDELEIRPNVYRNRIARQLNISLHSEFVYTDALAVAAQIFTAGIT 120
OY 121 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCIGEFVRKTLATWLRRGWTDVLCVY 180
DB 121 WGRVSLISYAAGLAVDCVHAOPAMVHTIVDCIGEFVRKTLATWLRKRGWMDITKCVY 180
OY 121 WGRVSLISYAAGLAVDCVHAOPAMVHTIVDCIGEFVRKTLATWLRKRGWMDITKCVY 180
DB 181 STDPGRSHMLVATLCSFGRLKAAPFLPPER 213
DB 181 STDPGRSHMLVAVNCSFGHFLKAIFFVLLPER 213

RESULT 5
OY 09DGJ5 PRELIMINARY; PRT; 213 AA.
AC 09DGJ5;
DB 01-MAR-2001 (TREMBLrel. 16, Created)
DB 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB Bcl-2-related ovarian killer protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Mills E.M., Johnson A.L., Bridgham J.T.;
RT "Characterization and Expression of Bok in the Hen Ovary.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF290888; AAG01182.1;
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR002475; BCL2_FAMILY.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SO SEQUENCE 213 AA; 23658 MW; 07CC06BBD7311EC CRC64;

Query Match
  Best Local Similarity 78.9%; Score 868; DB 13; Length 213;
  Matches 162; Conservative 23; Mismatches 28; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAALGREYVHARLLRAGLSMSAPERASAP 60
DB 1 MEVLRRSSVFAAEVMEFDRSPDKELVSOAKALCRDIYNSRLIRAGVSMKPEHNPVP 60
OY 61 GGRLAECVTLRLGDELLEQIRSVYRNVARQLHIPLQSEPVYTDALAVAGHIFSAGIT 120
DB 61 GGRLAECVTLRLGDELEIRPNVYRNRIARQLNISLHSEFVYTDALAVAAQIFTAGIT 120
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DB 61 GGRLAECVTLRLGDELEIRPNVYRNRIARQLNISLHSEFVYTDALAVAAQIFTAGIT 120
OY 121 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCIGEFVRKTLATWLRRGWTDVLCVY 180
DB 121 WGRVSLISYAAGLAVDCVHAOPAMVHTIVDCIGEFVRKTLATWLRKRGWMDITKCVY 180
OY 181 STDPGRSHMLVATLCSFGRLKAAPFLPPER 213
DB 181 STDPGRSHMLVAVNCSFGHFLKAIFFVLLPER 213

RESULT 6
OY 088857 PRELIMINARY; PRT; 170 AA.
AC 088857;
DB 01-NOV-1998 (TREMBLrel. 08, Created)
DB 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB Bcl-2-related ovarian killer protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=98024143; PubMed=9356461;
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;
RT "Bcl-2 is a pro-apoptotic bcl-2 protein with restricted expression in
RT reproductive tissues and heterodimerizes with selective anti-apoptotic
RT bcl-2 family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Hsu S.Y., Hsueh A.J.W.;
RT "A splicing variant of the Bcl-2 member Bok with a truncated BH3
RT domain induces apoptosis without dimerization with anti-apoptotic Bcl-
RT 2 proteins.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF051093; AAC61928.1;
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR002475; BCL2_FAMILY.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SO SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

Query Match
  Best Local Similarity 75.3%; Score 828.5; DB 11; Length 170;
  Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

OY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAALGREYVHARLLRAGLSMSAPERASAP 60
DB 1 MEVLRRSSVFAAEIMDAFDRSPDKELVSOAKALGREYVHARLLRAGLSMSAPERASAP 60
OY 61 GGRLAECVTLRLGDELLEQIRSVYRNVARQLHIPLQSEPVYTDALAVAGHIFSAGIT 120
DB 61 GGRLAECVTLRLGDELEIRPNVYRNRIARQLNISLHSEFVYTDALAVAAQIFTAGIT 120
OY 121 WGRVSLISYAAGLAVDCVQAOPAMVHALVDCIGEFVRKTLATWLRRGWTDVLCVY 180
DB 121 WGRVSLISYAAGLAVDCVHAOPAMVHTIVDCIGEFVRKTLATWLRKRGWMDITKCVY 180
OY 181 STDPGRSHMLVATLCSFGRLKAAPFLPPER 213
DB 181 STDPGRSHMLVAVNCSFGHFLKAIFFVLLPER 213

RESULT 7
OY 09V9C8 PRELIMINARY; PRT; 300 AA.
ID 09V9C8
```



DE AT16536p.  
 GN BUFEY.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Chape M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nanco J., Pacleib J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL:AY075219; AAL68086.1; -  
 SQ SEQUENCE 299 AA; 33379 MW; 7FB125A6B7323B23 CRC64;

Query Match 21.7%; Score 238.5; DB 5; Length 299;  
 Best Local Similarity 31.1%; Pred. No. 4.6e-13;  
 Matches 66; Conservative 33; Mismatches 82; Indels 31; Gaps 8;

OY 25 KELVAQKALGREYHARLRAGL--SWSAPERASAPG---GRAEVCVTLRLGDEL 78  
 DB 87 QDIISQRCICGHIKRLRSGLFNKKLQIRISLIGSTSMGIYADVPAVOVLDEL 146  
 OY 79 EOIRPSYRNVAROL-----HIPLOSEPVTDAFLAVAGHIFSGITGWKVSLSXA 130  
 DB 147 ERHPRYNGVARQICRNPGGEHTP---DAVSLIGAAGRELFRVETLWSKVISLFAI 202  
 OY 131 AGLAVDCVROAPAMVHALVDCIGFVRKTLATWLRRCGW---TDVLKCVSTKPGF 186  
 DB 203 AGLAVDCVROAGHPEYLPKIMESVIEDLVPMINENGSWGINTHVLPTNSLNP-- 260  
 OY 187 RSHWLVAATL-CSPG-----RFLKAFFLLPE 212  
 DB 261 -LEMTLVLIGVFPGLILVPMILRFENLIVPK 291

## RESULT 9

O9NGX3 PRELIMINARY; PRT; 313 AA.  
 ID O9NGX3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Bcl-2-like protein BUFEY (Fragment).  
 GN BUFEY OR CG8238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20153510; PubMed-10684252;  
 RA Colussi P.A., Quin L.M., Huang D.C., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RT "Debel, a proapoptotic bcl-2 homologue, is a component of the  
 RT Drosophila melanogaster cell death machinery."  
 RL J. Cell Biol. 148:703-714(2000).  
 DR EMBL:AF237864; AAF4120.1; -  
 DR HSSP: 007817; 1MAZ.  
 DR FLYBase: FBgn0040491; BUFEY.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PSS0062; BCL2\_FAMILY; 1.  
 FT NON TER 1  
 SQ SEQUENCE 313 AA; 34909 MW; 775A41FDD5B678E CRC64;

Query Match 21.7%; Score 238.5; DB 5; Length 313;  
 Best Local Similarity 31.1%; Pred. No. 4.6e-13;  
 Matches 66; Conservative 33; Mismatches 82; Indels 31; Gaps 8;

OY 25 KELVAQKALGREYHARLRAGL--SWSAPERASAPG---GRAEVCVTLRLGDEL 78  
 DB 101 QDIISQRCICGHIKRLRSGLFNKKLQIRISLIGSTSMGIYADVPAVOVLDEL 160  
 OY 79 EOIRPSYRNVAROL-----HIPLOSEPVTDAFLAVAGHIFSGITGWKVSLSXA 130  
 DB 161 ERHPRYNGVARQICRNPGGEHTP---DAVSLIGAAGRELFRVETLWSKVISLFAI 216  
 OY 131 AGLAVDCVROAPAMVHALVDCIGFVRKTLATWLRRCGW---TDVLKCVSTKPGF 186  
 DB 217 AGLAVDCVROAGHPEYLPKIMESVIEDLVPMINENGSWGINTHVLPTNSLNP-- 274  
 OY 187 RSHWLVAATL-CSPG-----RFLKAFFLLPE 212  
 DB 275 -LEMTLVLIGVFPGLILVPMILRFENLIVPK 305

## RESULT 10

O9V612 PRELIMINARY; PRT; 247 AA.

ID O9V612;  
 AC O9V612;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE CG8238 protein.  
 GN BUFEY OR CG8238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sulten G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrit J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
DR EMBL: AE003825; AAF58628.1; -  
DR HSSP: O07817; 1MA2  
DR FlyBase: FBgn0040491; Buffy.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
SO SEQUENCE 247 AA; 27466 MW; A2C4325AF4C1620 CRC64;

Query Match 20.9%; Score 230; DB 5; Length 247;  
Best Local Similarity 33.3%; Pred. No. 2e-12;  
Matches 54; Conservative 28; Mismatches 62; Indels 18; Gaps 4;

OY 25 KEIVAAQALGFEVYHARLRAGL--SMSAPRASPARG---GRLAECYVLLRLGDEL 78  
DB 87 ODIISGRCICGHYIKRRLRSGLFNKILGLQIRISLSTMGIVRDVFPAYQVYLGDEL 146  
OY 79 EOIRSVYRNVAROL-----HIPLQSEPVYTDAPLAVAGHIFSAGITGKVSLSYA 130  
DB 147 ERMHRIITNGVARQICRNPGGEFHP----DAVSLLGAVGELRVELTMSKVSLSRAI 202  
OY 131 AAGLAVDCVQAQAPAMVHALVDCLEFVRKLTATVLRKRGW 172  
DB 203 AGGLSVDCVRQGHPEYLPRLMESVEVIDELVPMINENGW 244

## RESULT 11

ID Q95083 PRELIMINARY; PRT; 317 AA.  
AC Q95083;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE GH01265P.  
GN DEBCL OR CG12397.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,  
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY058249; AAL13478.1; -  
DR FlyBase: FBgn0028131; debcl.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL; 1.  
SO SEQUENCE 317 AA; 34649 MW; 46B22FED1CC6F01F CRC64;

Query Match 19.0%; Score 209.5; DB 5; Length 317;  
Best Local Similarity 34.4%; Pred. No. 1.7e-10;  
Matches 54; Conservative 28; Mismatches 64; Indels 11; Gaps 5;

OY 26 ELVAAKALGFEVYHARLRAG-LSMSAPER---ASPARGRLAEVCYVLLRLGDEL 80  
DB 96 DIINGKCLCGGYTARLRAGVLRKVTQRLRLTLDPSSHVVEVPALMSKEELER 155  
OY 81 IRPSVYRNVAROL-HIP---LQSEPVYTDAPLAVAGHIFSAGITGKVSLSYAAGLAV 136  
DB 156 MHPRYTINISRLSRAPGCELESDMAPMLNLVAKDLFRSSITMGKIISITAVCGGFAI 215

OY 137 DCVROAQPAMVHALVDCLEFVRK--TLATWLRRCG 171  
DB 216 DCVROGHEDYDCLIDGLAEITGRGLADRRQRMVG 252

## RESULT 12

ID Q923R6 PRELIMINARY; PRT; 236 AA.  
AC Q923R6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE B-cell lymphoma protein 2.  
GN BCL2.  
OS *Cricetus longicaudatus* (Long-tailed hamster) (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC *Cricetus*.  
OX NCBI\_TaxID=10030;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Lai D.Z., Chen W., Wang H.T.;  
RT "Construction of a robust CHO cell line for biopharmaceutical use."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF043339; AAK92201.1; -  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH.  
DR InterPro: IPR002475; Bcl2\_FAMILY.  
DR InterPro: IPR004725; Bcl2\_reg.  
DR Pfam: PF00452; Bcl-2; 1.  
DR TIGRfams: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
DR PROSITE: PS01259; BH3; UNKNOWN\_1.  
DR PROSITE: PS01260; BH4\_1; UNKNOWN\_1.  
DR PROSITE: PS50063; BH4\_2; 1.  
SO SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match 14.4%; Score 158; DB 11; Length 236;  
Best Local Similarity 21.8%; Pred. No. 4e-06;  
Matches 47; Conservative 36; Mismatches 77; Indels 56; Gaps 7;

OY 28 VAQAKALG-----REYVHARLRAGLSW-----SAPERASPARG----- 61  
DB 1 MAOAGRTGYDNRKIYMKYIHYKLSORGYEMDVGDVADAPLGAAPPGIFSFQPSNPYPA 60  
OY 62 -----GRLAECYVLLRLGDELEQIRSVYRNVAR-----OLHT-P 96  
DB 61 VHRDMAARTSPLRPIVATGTGPLSPVPVHLTLRRAGDDFSRRYRDPFAEMSSQLHLTP 120  
OY 97 LQSEPVYTDAPLAVAGHIFSAGITGKVSLSYAAGLAVDCVROAQPAMVHALVDCLE 156  
DB 121 FTAR----GRFATVVEELFRDGVNMGRIVAFPEBGWCVESVNRKEMSPYDNLAMWTE 176  
OY 157 FVRKLTATVLRKRGWTDLCV-VSTRKPGFRSHWL 191  
DB 177 YLNRHLHTWIDONGMDAFVELYGPSVRPLDFESWL 212

## RESULT 13

ID Q35843 PRELIMINARY; PRT; 235 AA.  
AC Q35843;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Bcl-2-gamma.  
GN BCL2L.  
OS *Mus musculus* (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.







GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 7.50783 Seconds  
(without alignments)  
1176.699 Million cell updates/sec

Title: US-09-682-667-6  
Perfect score: 1100  
Sequence: 1 MEVLRRSSVFSAEIMDAFDR.....TLCSEGRFLKAFELLPER 213

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	167.5	15.2	236	1	BCI2_RAT
2	164.5	13.0	229	1	BCI2_BOVIN
3	159.5	14.5	236	1	BCI2_CRITO
4	157.5	14.3	236	1	BCI2_MOUSE
5	155	14.1	228	1	ARL_XENLA
6	155	14.1	233	1	BCI2_CHICK
7	153.5	14.0	239	1	BCI2_HUMAN
8	150.5	13.7	233	1	BCI2_MOUSE
9	150.5	13.7	233	1	BCI2_RAT
10	148.5	13.5	218	1	BAXB_HUMAN
11	146.5	13.3	233	1	BCI2_HUMAN
12	146.5	13.3	233	1	BCI2_PIG
13	143.5	13.0	192	1	BAXA_HUMAN
14	138.5	12.6	204	1	ARL1_XENLA
15	137.5	12.5	229	1	BCI2_CHICK
16	134.5	12.2	193	1	BCI2_MOUSE
17	133.5	12.1	192	1	BAXA_BOVIN
18	130.5	11.9	193	1	BCI2_HUMAN
19	129.5	11.8	192	1	BAXA_MOUSE
20	129.5	11.8	192	1	BAXA_RAT
21	128	11.6	208	1	BAK_MOUSE
22	127.5	11.6	211	1	BAK_HUMAN
23	122.5	11.1	211	1	BAK2_HUMAN
24	116	10.5	350	1	MCIL_HUMAN
25	110.5	10.0	143	1	BAID_HUMAN
26	97.5	8.9	115	1	CARB_MYCTU
27	95.5	8.7	172	1	BFL1_MOUSE
28	91.5	8.3	175	1	BFL1_HUMAN
29	88.5	8.0	1121	1	CARB_MYCTE
30	85.5	7.8	2003	1	NTC4_HUMAN
31	85	7.7	551	1	SMA4_MOUSE
32	85	7.7	552	1	SMA4_HUMAN
33	85	7.7	552	1	SMA4_PIG

34	85	7.7	552	1	SMA4_RAT	070437 rattus norv
35	84	7.6	941	1	DNAB_RHOMR	030477 rhodothermu
36	83	7.5	177	1	NR13_COTJA	090343 coturnix co
37	82.5	7.5	535	1	SSDH_HUMAN	P51649 homo sapien
38	82.5	7.5	1081	1	CARB_SYN73	Q55756 synchocyst
39	80.5	7.3	319	1	MOCB_SYN7	Q56208 synchococc
40	80.5	7.3	372	1	GDF1_HUMAN	P27539 homo sapien
41	80.5	7.3	385	1	RURE_PSEOL	P17052 pseudomonas
42	79.5	7.2	406	1	MCAL_SALRY	P26388 salmoneella
43	79.5	7.2	672	1	ACSA_PHYBL	001576 phycomyces
44	78.5	7.1	1075	1	CNRA_ALCEU	P37972 alcaaligenes
45	77	7.0	205	1	GTS1_ASCSU	P46436 ascaris suu

## ALIGNMENTS

RESULT 1	ID	BCI2_RAT	STANDARD:	PRT:	236 AA.
AC	P49950:	062837:	064032:		
DT	01-OCT-1996	(Rel. 34,	Created)		
DT	01-NOV-1997	(Rel. 35,	Last sequence update)		
DT	15-JUN-2002	(Rel. 41,	Last annotation update)		
DE	Apoptosis regulator Bcl-2.				
GN	BCL2 OR BCL-2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
NC	NCBI_TaxID=10116;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RA	MEDLINE=94193015; PubMed=8144041;				
RT	Sato T., Irie S., Krajewski S., Reed J.C.;				
RL	"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";				
RN	Gene 140:291-292(1994).				
[2]					
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Sprague-Dawley; TISSUE=ovary;				
RA	MEDLINE=95129487; PubMed=7828536;				
RT	Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;				
RL	"Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xl mRNA levels.";				
RT	Endocrinology 136:232-241(1995).				
[3]					
RP	SEQUENCE OF 19-172 FROM N.A.				
RA	MEDLINE=95059917; PubMed=7969891;				
RT	Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H., Lindholm D.;				
RL	"bcl-2 messenger RNA is localized in neurons of the developing and adult rat brain.";				
RT					
RL	Neuroscience 61:165-177(1994).				
CC	-I- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).				
CC	-I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BCL-XL. Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity).				
CC	-I- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.				
CC	-I- TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal				



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CC -----
DR EMBL: U92434; AAB53319.1; -
DR HSSP: 007817; 1MAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PR02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFS: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1; 1.
DR PROSITE: PS50063; BH4-2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10 30 BH4.
FT DOMAIN 64 68 POLY-PRO.
FT DOMAIN 69 72 POLY-ALA.
FT DOMAIN 83 97 BH3.
FT DOMAIN 126 145 BH1.
FT DOMAIN 177 192 BH2.
FT TRANSMEM 202 223 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 229 AA; 25099 MW; ADIDD0MF9BEFFILD CRC64;

Query Match 15.0%; Score 164.5; DB 1; Length 229;
Best Local Similarity 23.1%; Pred. No. 1.1e-07;
Matches 49; Conservative 36; Mismatches 76; Indels 51; Gaps 7;

QY 37 EYVHARLRLRGLSW-----SAPERASPARG-----GRAAE----- 66
DB 17 KYIHYKLSQGYEMDAGADAGAPGAPGAPGILSSQGRTPAPSRTPPPPPAAAGPAP 76
QY 67 -----VCVTLRLRDELQIRPSVYRNVAROLHI-PLQSEPVYTDALFVAGHIFSA 119
DB 77 SPFPVYVHLTLROAGDDFSRRYRRDRFAEMSSQLHLPTFKR-----EFATVVEELFPDGV 132
QY 120 TWGKVVSLXSAAGLAVDCVROAPAVNALVDCLGFEVKRTLATWLRGWTDLKCV 179
DB 133 NMGRIVAFEEFGVGCESVNREMSPLVDSIALMWTGYLRHLHTWQDNGMDAFVELY 192
QY 180 -VSTKGFGRSHMLVATLCSGRFLKAAFFLL 210
DB 193 GFSMRPLDFFSWL-----SLKALLSLAL 215

RESULT 3
BCL2_CRITO STANDARD; PRT; 236 AA.
ID BCL2_CRITO
AC Q9JUV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC Cricetus.
OX NCBI_TaxID=10030;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=20431763; PubMed=10973819;
RA Tomicic M.T., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT protein.";
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).

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RN [2]
RP SEQUENCE FROM N.A. AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=11181062;
RA Tomicic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT and caspase-3.";
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAIF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC (By similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC or send an email to license@sdb.ch).
CC EMBL: AJ271720; CAB92245.1; -
DR HSSP: 007817; 1MAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PR02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFS: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1; 1.
DR PROSITE: PS50063; BH4-2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10 30 BH4.
FT DOMAIN 64 68 BH3.
FT DOMAIN 69 72 BH1.
FT DOMAIN 133 152 BH2.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

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SQ SEQUENCE 236 AA; 26491 MW; BECADPFEF337228 CRC64;  
 Query Match 14.5%; Score 159.5; DB 1; Length 236;  
 Best Local Similarity 22.4%; Pred. No. 3e-07;  
 Matches 50; Conservative 37; Mismatches 79; Indels 57; Gaps 8;

QY 28 VQAQKALG-----KEYVHARLRLRGLSW-----SAPERASPAG----- 61  
 DB 1 MAQAGTGTGDNREIYMKYHYKISQGYEMDVGDDAALGAPRGIFSPQESNPTRA 60  
 QY 62 -----GRLAEVCTVLRIGDELEQIRPSVYRNVAR-----QLHI-P 96  
 DB 61 VHRDMAFRSPLRIVATGPTLSPVPVYVHLTLRRAGDQFSRRYRDFAEMSSQHLTP 120  
 QY 97 LOSEPVTDAFLAVAGHITSAGITGKVVSLYSAAGLAVDCVQAQAPMVAHALDCLGE 156  
 DB 121 FTAR-----GRFAIVVELEFRDGMGCRIVAFEFEGVCMCEVSNNRMSPLVDNALMPE 176  
 QY 157 FVRKTLATWLRRRGCGWTDVLCV-VSTRKGFPSHML-VATLCS 197  
 DB 177 YLNRHLHTWIDNGMDAFVELYGPSPVRLPDRFSWLSTLTL 219

## RESULT 4

BCL2\_MOUSE  
 ID BCL2\_MOUSE STANDARD; PRT; 236 AA.  
 AC P10417; P10418;

DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC STRAIN-BALB/C; TISSUE-Liver;  
 RX MEDLINE=87187643; PubMed=3032455;  
 RA Negtini M., Sillini E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of bcl-2: structure and expression of the murine  
 RT gene homologous to the human gene involved in follicular lymphoma.";  
 RL Cell 49:455-463(1987).  
 RN [2]  
 RP REVISIONS TO 221-222.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
 RX MEDLINE=97277291; PubMed=9115213;  
 RA "Ito T., Deng X., Carr B., May W.S. Jr.;  
 RT "Bcl-2 phosphorylation required for anti-apoptosis function.";  
 RL J. Biol. Chem. 272:11671-11673(1997).  
 RN [4]  
 RP DEPHOSPHORYLATION BY PP2A.  
 RX MEDLINE=99069407; PubMed=9852076;  
 RA Deng X., Ito T., Carr B., Mummy M., May W.S. Jr.;  
 RT "Reversible phosphorylation of Bcl2 following Interleukin 3 or  
 RT bryostatins 1 is mediated by direct interaction with protein  
 RT phosphatase 2A\*";  
 RL J. Biol. Chem. 273:34157-34163(1998).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).

CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (by  
 CC domains). Also interacts with APAF-1 and RAIF-1.  
 CC -1- SIMILARITY: Also interacts with APAF-1 and RAIF-1.  
 CC -1- SUPCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAIF-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- Dephosphorylated by protein phosphatase 2A (PP2A).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L31532; AAA37282.1; -  
 DR EMBL: M16506; AAA37282.1; JOINED.  
 DR EMBL: M16506; AAA37281.1; -  
 DR PIR: A25960; TVMSA1.  
 DR PIR: B25960; TVMSA1.  
 DR PIR: E37332; E37332.  
 DR HSSP: 007817; IMA2.  
 DR MGD: MGI:88138; Bcl2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR007112; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS01260; BH4-1; 1.  
 DR PROSITE: PS50063; BH4-2; 1.  
 DR Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;  
 KW phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC).  
 FT VARSPPLIC 193 236 DAFVELGSPSRPLPDEFSELTKTLTSLALVACITLGAAYL  
 FT GHK -> VGACILE (IN ISOFORM BETA).  
 SQ SEQUENCE 236 AA; 26425 MW; AA85FE6B0766BE0A CRC64;  
 Query Match 14.3%; Score 157.5; DB 1; Length 236;

Best Local Similarity 22.4%; Pred. No. 4.6e-07;  
Matches 50; Conservative 37; Mismatches 79; Indels 57; Gaps 8;

OY 28 VQAQKALG-----REYVAKRLRLAGLSW-----SAPRRASAPRG-----61  
Db 1 MAQAGRGYDNRREIVMKYIHYKLSORGEWDADADADAPLGAAPPGCIFSFOESNMPA 60  
OY 62 -----GRLAEVCTVLLRLDELEQIRPSYRVNAR-----QLHI-P 96  
Db 61 VHEEMAKRISPLRLPVATAGPALSPPVPCVHLTLRRAGDPSRRYRRDFAMSSQLHLTP 120  
OY 97 LQSEPVVTDAPFLAVAGHIFSAGITWCKVSLYSAAAGLAVDCVROAPAMVHALVDCLGE 156  
Db 121 FTAR-----GREATVEELFRDGVNMGRIVAFEEFGVGVCESVNREKSPLVNDIALMTE 176  
OY 157 FVKRTLATWLRBRGGWTDVLCV-VSTKPGFRSHML-VAILCS 197  
Db 177 YLNRHLHTWIDNGMDAFVELYGPSMRPLDFESWLSKTLIS 219

## RESULT 5

ARL\_XENLA ID STANDARD; PRT; 228 AA.  
AC 091827;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator B1 (XRL) (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodinae; Xenopus.  
NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head;  
RX MEDLINE=95331613; PubMed=7607538;  
RA Cruz-Reyes J., Tata J.R.;  
RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
RT cell-survival genes".  
RT Gene 158:171-179(1995).  
CC -1- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
CC ADULTS. WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X82462; CA57845.1; -  
DR HSSP: Q07817; IMAZ.  
DR InterPro: IPR002475; BCL2\_family.  
DR InterPro: IPR000712; BCL2\_BH.  
DR InterPro: IPR003093; BCL2\_BH4.  
DR Pfam: PF00452; BCL-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART: SM00337; BCL; 1.  
DR SMART: SM00265; BH4; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01258; BH2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR Apoptosis; Transmembrane.  
KW NON\_TER 1  
FT DOMAIN 120 139 BH1.

FT DOMAIN 171 186 BH2.  
FT TRANSMEM 207 227 POTENTIAL.  
SQ SEQUENCE 228 AA; 25068 MW; C499DD449A585F8A9 CRC64;

Query Match 14.1%; Score 155; DB 1; Length 228;  
Best Local Similarity 23.6%; Pred. No. 7.4e-07;  
Matches 39; Conservative 35; Mismatches 71; Indels 20; Gaps 5;

OY 19 DRMPDQKELVQA-----AKALGREYVAKRLRLAGLSWAPRRASAPRGRLAELVC---TVL 71  
Db 32 DKYITEGGMAAQSDLGSRALVEDLVRYKLCORSL-----VPEPSG--AASCAHSAM 81  
OY 72 LRLGDELEQIRPSYRVNARQLHPILOSEPVVTDAPFLAVAGHIFSAGITWCKVSLYSAA 131  
Db 82 RAODEFEERFRQAFSPISQIHV---TPGTARAFELVAGSLFQGVNMGRIVAFRVFG 138  
OY 132 AGLAVDCVROAPAMVHALVDCGEEVFKRTLATWLRBRGGWTDVL 176  
Db 139 AALCAESVNKEMSPLLPRIDMMVTVLETNLRDVIQNGMGNGPL 183

## RESULT 6

BCL2\_CHICK ID STANDARD; PRT; 233 AA.  
AC 000709;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2 OR BCL-2.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92375724; PubMed=1508712;  
RA Ezuchl Y., Ewert D.L., Tsujimoto Y.;  
RT "Isolation and characterization of the chicken bcl-2 gene: expression  
RT in a variety of tissues including lymphoid and neuronal organs in  
RT adult and embryo".  
RT Nucleic Acids Res. 20:4187-4192(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell lymphoma;  
RX MEDLINE=92379084; PubMed=1511008;  
RA Cazals-Hatem D.L., Louie D.C., Yanaka S., Reed J.C.;  
RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken  
RT homologue of the Bcl-2 oncoprotein".  
RT Biochim. Biophys. Acta 1132:109-113(1992).  
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (ApAF-1).  
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
CC domains, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with ApAF-1 and ApAF-1 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,  
CC kidney, heart, ovary and brain, with the highest levels in the  
CC thymus. In the embryo, highly levels expressed in all tissues with  
CC high levels in the bursa of Fabricius.  
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
CC for interaction with ApAF-1 (By similarity).  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: D11382; BAA01978.1;
DR EMBL: D11381; BAA01978.1; JOINED.
DR EMBL: Z11961; CA78018.1;
DR PIR: A37332; A37332.
DR PIR: S24390; S24390.
DR HSSP: Q07817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_Reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Transmembrane; Mitochondrion.
FT DOMAIN 10 30 BH4.
FT DOMAIN 87 101 BH3.
FT DOMAIN 130 149 BH1.
FT DOMAIN 181 196 BH2.
FT TRANSMEM 208 228 POTENTIAL.
FT CONFILCT 64 64 E -> S (IN REF. 2).
FT CONFILCT 67 82 GSAASEVPPAEGLRP -> ARLLVRCPRRLGCA
FT CONFILCT 121 121 (IN REF. 2).
FT CONFILCT 139 139 H -> T (IN REF. 2).
FT CONFILCT 139 139 G -> V (IN REF. 2).
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6EC3D CRC64;

Query Match 14.1%; Score 155; DB 1; Length 233;
Best Local Similarity 20.6%; Pred. No. 7.6e-07;
Matches 45; Conservative 36; Mismatches 81; Indels 56; Gaps 6;

OY 37 EYVHARLLRAGISWSA-----PERASPAAGGRLAEVCT----- 69
DB 17 KIYHKLSQKGYDMAAGDEPRPPVPAAPAAVAAGASSHHRPEPPGSAASEVPP 76
OY 70 -----VLLRLDELEQIRPSYRVNVARQLH-PLQSEPVYVDAFLAVAGHIF 115
DB 77 AEGLRPAPGVHIALRQAGDEFRRYQGRDEAQMGLHHTPTAH-----GRVAVAEELF 132
OY 116 SAGITWGKVVSLYSAAAGLAUDCVQAOAPAMVHALVDCIEGVVKTATLWLRRGQMTDV 175
DB 133 RDGVWNGRIVAFEEFEGVWCESVNRKSPLDNIAWTETELNHLNMIODNGMDAF 192
OY 176 LKCV-VSTRKPGFRSHW-----LVATLCSFGREL 202
DB 193 VELYGNMRLPFDPSWISLKTILSLVLVAGACITLGAAYL 230

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DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid-9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT 2/immunoglobulin transcript resulting from the t(14;18)
RT translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockelt R.D., Granger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-Ig fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE OF 1131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
RX MEDLINE=92096610; PubMed=1339299;
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT "Frequent incidence of somatic mutations in translocated BCL2
RT oncogenes of non-Hodgkin's lymphomas.";
RL Blood 79:229-237(1992).
RN [6]
RP SUBCELLULAR LOCATION.
RX MEDLINE=91066924; PubMed=2250705;
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT programmed cell death.";
RL Nature 348:334-336(1990).
RN [7]
RP MUTAGENESIS.
RX MEDLINE=94239528; PubMed=8183370;
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT apoptosis and heterodimerization with Bax.";
RL Nature 369:321-323(1994).
RN [8]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RX MEDLINE=98057466; PubMed=9395403;
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
RA Ueno K., Hardwick J.M.;
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
RL Science 278:1966-1988(1997).
RN [9]
RP REVIEW ON PHOSPHORYLATION.
RX MEDLINE=21260650; PubMed=11368354;
RA Ruvoilo P.P., Deng X., May W.S.;
RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
RL Leukemia 15:515-522(2001).
RN [10]
RP PHOSPHORYLATION BY ASK1/JNK1.

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RX MEDLINE-20036804; PubMed-10567572;  
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
 RT "Bcl-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
 RT protein kinase pathway normally activated at G(2)/M.";  
 RL Mol. Cell. Biol. 19:8469-8478(1999).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with Apaf-1 and Raf-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with Raf-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- DISEASE: Involved in follicular Lymphoma (FL) (also known as type  
 CC t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene  
 CC regions.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -1- DATABASE: BELONGS TO THE BCL-2 FAMILY.  
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;  
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BCL2ID49.htm".  
 CC -----  
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 CC -----  
 CC EMBL: M13994; AAA51813.1; ALT\_SEQ.  
 CC EMBL: M13995; AAA51814.1; ALT\_SEQ.  
 CC EMBL: M14745; AAA35591.1; -  
 CC EMBL: X06487; CAA29778.1; -  
 CC EMBL: S72602; AAD14111.1; ALT\_SEQ.  
 CC PIR: A29409; TVHUB1.  
 CC PIR: B29409; TVHUB1.  
 CC PIR: A24428; TVHUBC.  
 CC PIR: C37332; C37332.  
 CC PIR: D37332; D37332.  
 CC HSSP: 007817; 1MAZ.  
 CC DR Genew: HGNC:990; BCL2.  
 CC DR MIM: 151430; -  
 CC DR InterPro: IPR002475; BCL2\_family.  
 CC DR InterPro: IPR000712; Bcl2\_BH.  
 CC DR InterPro: IPR003093; Bcl2\_BH4.  
 CC DR InterPro: IPR004725; Bcl2\_reg.  
 CC DR Pfam: PF00452; Bcl-2; 1.  
 CC DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00602; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4.1; 1.  
 DR PROSITE: PS00603; BH4.2; 1.  
 DR PROTO-ONCOGENE: Apoptosis; BH4.2; 1.  
 DR Mitochondrion; Phosphorylation; Chromosomal translocation;  
 KW Polymorphism; Disease mutation.  
 FT DOMAIN 10 30  
 FT DOMAIN 93 107  
 FT DOMAIN 136 155  
 FT DOMAIN 187 202  
 FT TRANSMEM 212 233  
 FT SITE 34 35  
 FT MOD\_RES 70 70  
 FT VARSPIC 196 239  
 FT VARIANT 7 7  
 FT VARIANT 59 59  
 FT VARIANT 59 59  
 FT VARIANT 93 93  
 FT VARIANT 93 93  
 FT MUTAGEN 34 34  
 FT MUTAGEN 64 64  
 FT MUTAGEN 145 145  
 FT MUTAGEN 188 188  
 FT CONFLICT 48 48  
 FT CONFLICT 59 59  
 FT CONFLICT 117 117  
 FT CONFLICT 129 129  
 FT SEQUENCE 239 AA; 26266 MW; 3C49F2B714DC9CBB CRC64;  
 Query Match 14.0%; Score 153.5; DB 1; Length 239;  
 Best local Similarity 21.9%; Pred. No. 1.1e-06;  
 Matches 46; Conservative 37; Mismatches 74; Indels 53; Gaps 7;  
 QY 37 EYVHARLRLRGLSM-----SAPERASPARC-----GRAEYCT-- 69  
 DB 17 KYIHVLSQRYGWDAGDVGAPGAPGAPGHTPHPAASRDVARTSPLOTTPA 76  
 QY 70 -----VLRLGDELEQIRSVYRNVARQLRI-PLQSEPVYTDFAFLA 109  
 DB 77 APCAAGPALSPVPVYVHLTLRQAGDPSRTRYRDRFAKMSQHLTPFTAR----GRFAT 132  
 QY 110 VAGHIFSAGITGKGVVSLYSAAAGLAVDCVQAQAPVHALVDLCGEFYKTLATMLRRR 169  
 DB 133 VVEELFRDGVNMGRIYVAFFEGGVCVESVNRMSPLVDNIALMTEYILRHILHTWIDN 192  
 QY 170 GSWTDVLKVC-VSTKPGFRRSHML-VATFICS 197  
 DB 193 GGDMAFVELYGPMSRPLPDEFMSLTKTLUS 222  
 RESULT 8  
 BCLX\_MOUSE  
 ID BCLX\_MOUSE STANDARD: PRT; 233 AA.  
 AC 064373; Q60657; Q60658; Q6138;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2AAB;  
RA Kanesaki H., Michaud G.Y., Takatsu K., Okuma M.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=95331139; PubMed=7607090;  
RA Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L.H.,  
RA Thompson C.B., Nunez G.;  
RT "bcl-XL is the major bcl-x mRNA form expressed during murine  
RT development and its product localizes to mitochondria.";  
RL Development 120:3033-3042(1994).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TW)).  
RC TISSUE=Pre-B cell;  
RX MEDLINE=95052604; PubMed=7963517;  
RA Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;  
RT "Cloning and molecular characterization of mouse bcl-x in B and T  
RT lymphocytes.";  
RL J. Immunol. 153:4388-4398(1994).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).  
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
RX MEDLINE=98051053; PubMed=9390687;  
RA Yang X.-F., Weber G.F., Cantor H.;  
RT "A novel Bcl-x isoform connected to the T cell receptor regulates  
RT apoptosis in T cells.";  
RL Immunity 7:629-639(1997).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97289584; PubMed=9144489;  
RA Grilhot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,  
RA Ohta S., Seldin M.F., Nunez G.;  
RT "Genomic organization, promoter region analysis, and chromosome  
RT localization of the mouse bcl-x gene.";  
RL J. Immunol. 158:4750-4757(1997).  
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
CC caspases (By similarity). Appears to regulate cell death by  
CC blocking the voltage-dependent anion channel (VDAC) by binding  
CC to it and preventing the release of the caspase activator,  
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S)  
CC isoform promotes apoptosis.  
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
CC similarity). Heterodimerization with BAX does not seem to be  
CC required for anti-apoptotic activity (By similarity).  
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
CC ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TW), BCL-X(S),  
CC BCL-X(BETA) AND BCL-X(DELTA-TW); ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. WITH HIGHEST LEVELS IN THE  
CC BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-  
CC TW) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN  
CC ACTIVATED.  
CC -1- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND  
CC POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN  
CC POSTNATAL TISSUES.  
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
CC The BH1 and BH2 domains are required for both heterodimerization  
CC with other Bcl2 family members and for repression of cell death.  
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By  
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
CC apoptotic activity (By similarity).  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X85874; CAA58557.1; -  
DR EMBL: L35049; AAA51039.1; -  
DR EMBL: L35048; AAA51040.1; -  
DR EMBL: U10102; AAA82174.1; -  
DR EMBL: U10101; AAA82173.1; -  
DR EMBL: U10100; AAA82172.1; -  
DR EMBL: U51279; AAC53460.1; -  
DR EMBL: U78031; AAB96881.1; -  
DR EMBL: U78030; AAB96881.1; JOINED.  
DR HSSP: P53563; IAF3.  
DR MGD: MGI:88139; Bcl2l.  
DR InterPro: IPR002475; Bcl2\_family.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH4.  
DR InterPro: IPR004725; Bcl2\_reg.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART: SM00337; BCL; 1.  
DR SMART: SM00265; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01258; BH2; 1.  
DR PROSITE: PS01259; BH3; 1.  
DR PROSITE: PS01260; BH4\_1; 1.  
DR PROSITE: PS50063; BH4\_2; 1.  
DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.  
FT DOMAIN 4 24 BH4.  
FT DOMAIN 86 100 BH3.  
FT DOMAIN 129 148 BH1.  
FT DOMAIN 180 195 BH2.  
FT TRANSMEM POTENTIAL.  
FT VARSPLIC 210 226 MISSING (IN ISOFORM BCL-X(S)).  
FT VARSPLIC 126 188 DFPVDLYGNNAAESRKGQEPNRFPLTGMVAGVLLGSL  
FT VARSPLIC 189 233 FSRK -> VRTTPLYCPPLACVSLCEHP (IN ISOFORM  
FT BCL-X(BETA)).  
FT VARSPLIC 194 233 LYGNNAAESRKGQEPNRFPLTGMVAGVLLGSLFSRK  
FT -> GHDCGMCQSGAGLTLLSEVTRH (IN ISOFORM BCL-  
FT X(DELTA-TW)).  
SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;  
Query Match 13.7%; Score 150.5; DB 1; Length 233;  
Best Local Similarity 22.1%; Pred. No. 1.9e-06;  
Matches 43; Conservative 29; Mismatches 68; Indels 55; Gaps 5;  
OY 23 TDKELVAQAKKALGREYVHARLLAGLSNS-----APER----- 56  
DB 4 SREELV-----DFLSKLSOKGYSWQSQSDVENRTAEETAEERPSAINGPS 56  
OY 57 -----SPAAGCR-----LAEVCTVLLRLGDELEIPRPSVRYNAROLHPL 97  
DB 57 WHLADSPANVANGTGHSSSLDAAREYIPMAAVKQALKEAGDEFLRARRAFSDLTSLHT-- 114  
OY 98 OSEPVYTDAAFLAVACHITSAGITGKVVSLVSAAGLAVDCYQAOPAMVHALVDCLGEF 157  
DB 115 -PPGAYOSFEQVVELFEDGVNMGRIYAFSFGALCVESYDKEMOVLVSRIASMATY 173  
OY 158 VKRTLATLWLRRGGW 172  
DB 174 LNDHLEPWIQENGW 188  
RESULT 9  
BCLX\_RAT BCLX\_RAT STANDARD; PRT; 233 AA.



DB 174 LNDHLEPMIOENGM 188

RESULT 10

ID	BAXB_HUMAN	STANDARD	PRT	218 AA
AC	007817			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Apoptosis regulator BAX, cytoplasmic isoform beta.			
GN	BAX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=93364978; PubMed=8358790;			
RA	Olival Z.N., Millman C.L., Korsmeyer S.J.;			
RT	"Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates programmed cell death.";			
RL	Cell 74:609-619(1993).			
CC	-1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADONOVIRUS HOMOLOG E1B 19K PROTEIN.			
CC	-1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.			
CC	-1- DOMAIN: INTERACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.			
CC	CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC	-----			
CC	CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: L22474; AAA03620.1; -			
DR	PIR: B47538; B47538.			
DR	HSSP: 007817; IMAZ.			
DR	Genew: HGNC:959; BAX.			
DR	MTM: 600040.			
DR	InterPro: IPR002475; BCL2_family.			
DR	InterPro: IPR000712; Bcl2_BH.			
DR	Pfam: PF00452; Bcl-2; 1.			
DR	SMART: SM00337; BCL; 1.			
DR	PROSITE: PS01080; BH1; 1.			
DR	PROSITE: PS01258; BH2; 1.			
DR	PROSITE: PS01259; BH3; 1.			
DR	PROSITE: PSS0062; BCL2_FAMILY; 1.			
DR	APOLITIS; Alternative splicing.			
FT	DOMAIN 59 73 BH3.			
FT	DOMAIN 98 118 BH1.			
FT	DOMAIN 150 165 BH2.			
SO	SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;			

Query Match 13.5%; Score 148.5; DB 1; Length 218;  
 Best Local Similarity 28.8%; Pred. No. 2,7e-06;  
 Matches 46; Conservative 29; Mismatches 72; Indels 13; Gaps 6;

DB 124 ALCTKVPFLITIMGTDLFRLRLGWIQDGGVRLK 163

RESULT 11

ID	BCLX_HUMAN	STANDARD	PRT	233 AA
AC	007817; 092976;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Apoptosis regulator Bcl-x.			
GN	BCL2L1 OR BCL2L OR BCLX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).			
RX	MEDLINE=93364977; PubMed=8358789;			
RA	Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,			
RA	Turka L.A., Mao X., Nunez G., Thompson C.B.;			
RT	"bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";			
RL	Cell 74:597-608(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA).			
RA	Inohara N., Ohta S.;			
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.			
RX	MEDLINE=95372373; PubMed=7644501;			
RA	Sedlak T.W., Olival Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,			
RA	Korsmeyer S.J.;			
RT	"Multiple Bcl-2 family members demonstrate selective dimerizations with Bax.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).			
RN	[4]			
RP	MUTAGENESIS OF BH1 AND BH2 DOMAINS.			
RX	MEDLINE=96170038; PubMed=859636;			
RA	Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,			
RT	Korsmeyer S.J.;			
RL	"Bax-independent inhibition of apoptosis by Bcl-XL.";			
RN	Nature 379:554-556(1996).			
RP	STRUCTURE BY NMR OF 1-209.			
RX	MEDLINE=97117562; PubMed=9020082;			
RA	Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,			
RA	Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,			
RA	Thompson C.B., Fesik S.W.;			
RT	"Structure of Bcl-XL-Bax peptide complex: recognition between regulators of apoptosis.";			
RL	Science 275:983-986(1997).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.			
RX	MEDLINE=9625675; PubMed=8692274;			
RA	Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,			
RA	Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,			
RA	Ng S.L., Fesik S.W.;			
RT	"X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed cell death.";			
RL	Nature 381:335-341(1996).			
RN	[7]			

RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.  
 RX MEDLINE-98118550; PubMed-9435230;  
 RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,  
 RA Takahashi A., Kasan M.B., Griffin D.E., Earshaw W.C., Veluona M.A.,  
 RA Hardwick J.M.,  
 RT "Modulation of cell death by Bcl-XL through caspase interaction."  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (by similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-X(S)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC Heterodimerization with BAX does not seem to be required for anti-  
 CC apoptotic activity.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS  
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING  
 CC LYMPHOCTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING  
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.  
 CC -1- DOMAIN: The B4 domain is required for anti-apoptotic activity.  
 CC The B1 and B2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the B4 domain, has pro-apoptotic  
 CC activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC or send an email to [license@isb-sid.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: 223116; CAA80662.1; -  
 DR EMBL: 223115; CAA80661.1; -  
 DR EMBL: U72398; AAB17354.1; -  
 DR PDB: 1BXL; 29-OCT-97.  
 DR PDB: 1LXL; 21-APR-97.  
 DR PDB: 1MAZ; 21-APR-97.  
 DR Genew: HGNC:992; BCL2L1.  
 DR MIM: 600039; -  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS0063; BH4\_2; 1.  
 DR Apoptosis: Mitochondrion; Alternative splicing; Transmembrane;  
 KW 3D-structure.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH1.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.  
 FT SITE 61 61 CLEAVAGE BY CASPASE-1.  
 FT VARSPIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 FT VARSPIC 189 233 DIVEYLGNNAAESRRGGRNREMLTGTVAGVLLGSL  
 FT ESKR -> VTRKPLVCPFLASGSRFTALLVFLCWVI  
 FT VGDVDS (IN ISOFORM BCL-X(BETA)).  
 FT D->A: NO CLEAVAGE BY CASPASE-1 NOR BY  
 FT CASPASE-3.  
 FT FRD->A: NO HETERO-DIMERIZATION WITH BAX.  
 FT VNM->A: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT GRI->ELN: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT G->A: NO HETERO-DIMERIZATION WITH BAX.  
 FT G->E: NO HETERO-DIMERIZATION WITH BAX.  
 FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY  
 FT BY ABOUT HALF.  
 FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT G->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT CONFLICT 70 70  
 FT SEQUENCE 233 AA; 26049 MR; E09D3CDD851AE9BE CRC64;  
 SO  
 QY 23 TDKELVAQAALGREYVHARLARGLSMS-----APEEA----- 56  
 Db 4 SNRELVV-----DELSTYLSQKGYMSQSFSDVENRENTAPEGTESEMETPSAINGNPS 56  
 QY 57 -----SPAPGGR-----LAECVTLLRLGDELEDIRSVYNNVAROLHPL 97  
 Db 57 WHLADSPAVNGAGCHSSLDAREVIPAAYKQALREAGDEFLRYRASFDLISQHLI-- 114  
 QY 98 QSEPVYTDALFVAGHIFSGITGKVVSLYSAAAGLAVDCVROAQDPAVYHALVDCGEF 157  
 Db 115 -TGTAYOSFEQVYNELFRDGVNMGRIVAFPSGALCVESYDKEMQVLSRIANMATY 173  
 QY 158 VRKTLATWLRRRGGW 172  
 Db 174 LNDHLEPWIQENGW 188  
 RESULT 12  
 BCLX.PIC STANDARD; PRT; 233 AA.  
 ID BCLX.PIC  
 AC 07737;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99171363; PubMed-10072723;  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Diermer D.;  
 RT "Quantification of cardioprotective gene expression in porcine  
 RT short-term hibernating myocardium".  
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (by similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane.  
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (by similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR

CC ENVELOPE (BY SIMILARITY).  
 CC -I- DOMAIN: The Bcl2 domain is required for anti-apoptotic activity.  
 CC The Bcl1 and Bcl2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -I- PPM: Prototypically cleaved by caspases during apoptosis (by  
 CC similarity). The cleaved protein, lacking the Bcl4 domain, has pro-  
 CC apoptotic activity (by similarity).  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC -----  
 CC EMBL: AJ001203; CAA04597.1; -  
 CC HSSP: Q07817; 1MA2.  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01359; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS00063; BH4\_2; 1.  
 DR Apoptosis; Mitochondrion; Transmembrane.  
 KM DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 SQ SEQUENCE 233 AA: 26061 MM: 185F6FA0441912B2 CRC64;  
 Query Match 13.3%; Score 146.5; DB 1; Length 233;  
 Best Local Similarity 22.1%; Pred. No. 4.3e-06;  
 Matches 43; Conservative 29; Mismatches 68; Indels 55; Gaps 5;  
 OY 23 TRKELVAKKALGREYVHARLRAGLSWS-----APERA----- 56  
 DB 4 SNRELIV-----DFLSYKLSQKGSWSQFDVEENRTAEDEGESEAEFSAINGNPS 56  
 OY 57 -----SPARGR-----LAECVTLRLGDELDIRSVRYNAROLHPL 97  
 DB 57 WILADSPAYNGATGSSSIDAREVTPMAVYKQALRPRAGEFELRRRAISDLISQHL-- 114  
 OY 98 OSEPVVTDALAVAGHIFSGITWGVSLVSAAGLAVDCVROAPAVVHNLVDCIGEF 157  
 DB 115 -PPGAYGSEFEQVNLNLFEDGVNMGRIVAFSFGALCVESDKENQVLSIATIMATY 173  
 OY 158 VKTTLATWLRRCGW 172  
 DB 174 LNDHLEPWTQENGW 188  
 RESULT 13  
 BAXA\_HUMAN  
 ID BAXA\_HUMAN STANDARD: PRT; 192 AA.  
 AC Q07812;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, membrane isoform alpha.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-B-cell;  
 RC MEDLINE=93364978; PubMed=8358790;  
 RX Olvay Z.N., Millman C.L., Korsmeyer S.J.;  
 RA "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
 RT accelerates programmed cell death.";  
 RL Cell 74:609-619(1993).  
 RN [2]  
 RP MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.  
 RX MEDLINE=96091131; PubMed=8521816;  
 RA Chitenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,  
 RA Elangovan B., Chinnadurai G., Lutz R.J.;  
 RA "A conserved domain in Bax, distinct from Bcl1 and Bcl2, mediates cell  
 RT death and protein binding functions.";  
 RL EMBO J. 14:5589-5596(1995).  
 RN [3]  
 RP VARIANT PLASMACYTOMA GLU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC  
 RP LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.  
 RX MEDLINE=98200607; PubMed=9531611;  
 RA Meijerink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,  
 RA Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;  
 RA "Hematopoietic malignancies demonstrate loss-of-function mutations of  
 RT BAX.";  
 RL Blood 91:2991-2997(1998).  
 CC -I- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS  
 CC HOMOLOG B19 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,  
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.  
 CC -I- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
 CC B19 19K PROTEIN, BCL-X(L), MCL-1 AND A1.  
 CC -I- SUBCELLULAR LOCATION: Membrane-bound.  
 CC -I- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
 CC ALTERNATIVE SPLICING.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -I- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC -I- APOPTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC -I- DISEASE: Defects in BAX are found in some cell lines from  
 CC hematopoietic malignancies as T-cell acute lymphoblastic leukemia,  
 CC Burkitt lymphoma, and plasmacytoma.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC -----  
 CC EMBL: L22473; AAA03619.1; -  
 DR PIR: A47538; A47538.  
 DR HSSP: Q07817; 1MA2.  
 DR Genew: HGNC:959; BAX.  
 DR MIM: 600040;  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.



```
CC DEVELOPMENT.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTRACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
DR EMBL: Z23110; CAA80657.1; -.
DR EMBL: U26645; AAB07677.1; -.
DR PIR: A47537; A47537.
DR HSSP: P53563; IAF3.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis: Transmembrane; Alternative splicing.
DR DOMAIN 4 24 BH4.
FT DOMAIN 82 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223 POTENTIAL.
FT VARSPIC 185 229 ERFVLDYGNNAAEALRKGOETPFNKILTGATVAGVLLGLSL
SO SEQUENCE 229 AA: 25733 MW: A97D3A4D04C0E9DA CRC64;
LSRK-> VRRALP (IN SHORT ISOFORM).

Query Match 12.5%; Score 137.5; DB 1; Length 229;
Best Local Similarity 22.0%; Pred. No. 2.7e-05;
Matches 42; Conservative 30; Mismatches 68; Indels 51; Gaps 5;

OY 23 TDKELVQAQAKLGRVYHARLLRAGLSWAPD-----RASPA---P 60
DB 4 SNRELVI-----DFVSYKLSORCHCWESELEEDENRTDTAAEAEMDSVLNGSPSWHP 56
OY 61 GG-----RLAEVCVLLRLGDELEQIRPSVYRNVARQLHPILOSEP 101
DB 57 AGHYVNGATVYRRSSLEVHEIYRASVDVROALRDAGDEFELRYRRAPSDLTSLHT--TPG 113
OY 102 VTTDAFLAVACHISAGITGCKVSVLSAAGLAVDCYRQAPAMVHALVDCLIGEFVRKT 161
DB 114 TAYQSFEGVAVNELFHDGVNMGRIYAFSFGALCVESVDKEMRVLYGRIVSMVTYTLTDH 173
OY 162 LATWLRRRGGM 172
DB 174 LDPWIOENGW 184
```

Search completed: April 29, 2003, 11:23:56  
Job time : 8.50783 secs



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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 13.3473 Seconds  
(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-6

Perfect score: 1100

Sequence: 1 MEVLRSSVFPAEIMDAFDR.....TLCFGRFLKAFILLPER 213

Scoring table: BIOSUM62  
Gapop 10.0 , Gaepct 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164.5	15.0	236	2 I53744	gene bcl-2 protein
2	159.5	14.5	236	2 JC7383	B-cell lymphoma 2
3	159	14.5	236	2 I67432	BCL-2 - rat (fragm
4	158.5	14.4	227	2 JE0203	apoptosis regulato
5	157.5	14.3	236	1 TVMSA1	transforming prote
6	156	14.2	216	2 B37332	transforming prote
7	155	14.1	233	2 A37332	transforming prote
8	153.5	14.0	239	1 TVHUA1	transforming prote
9	151.5	13.8	232	2 S24390	transforming prote
10	150.5	13.7	199	1 TVMSB1	transforming prote
11	150.5	13.7	214	2 I49057	bcl-x transmembran
12	150.5	13.7	233	2 I49056	bcl-x long - mouse
13	149.5	13.6	233	2 S51761	BCL-X protein - ra
14	148.5	13.5	218	2 B47538	bcl-2-associated p
15	148	13.5	233	2 I67431	BCL-X-long - rat
16	146.5	13.3	233	2 B47537	apoptosis regulato
17	145.5	13.2	179	2 JC7255	Bax-delta protein
18	145.5	13.2	205	1 TVHUB1	transforming prote
19	143.5	13.0	192	2 A47538	bcl-2-associated p
20	137.5	12.5	190	2 A47537	apoptosis regulato
21	127.5	11.6	192	2 D47538	bcl-2-associated p
22	127.5	11.6	211	2 S58873	Bak protein - huma
23	123	11.2	133	2 I53295	bcl-2-associated p
24	122.5	11.1	211	2 S58875	cdn-2 protein - hu
25	120	10.9	350	2 A47476	BCL2 homolog MCL1
26	110.5	10.0	143	2 I38921	bcl-2-associated p
27	105	9.5	154	2 I58194	gene bcl-2 protein
28	97.5	8.9	115	2 A70990	carbamoyl-phosphat
29	95.5	8.7	172	2 I49449	hemopoietic-specif

30	94.5	8.6	1203	2 I55466	N-methyl-D-asparta
31	92	8.4	860	2 C82750	mannosyltransferas
32	91.5	8.3	175	2 I39055	Bcl-2 related - hu
33	90.5	8.2	118	2 S70089	kora protein - Amy
34	89	8.1	411	2 E70667	hypothetical prote
35	88.5	8.0	1129	2 H86975	probable carbamoyl
36	87	7.9	373	2 H84404	ferrichrome ABC tr
37	85.5	7.8	600	2 D87232	conserved membrane
38	85	7.7	552	2 S71811	probable transcrip
39	83	7.5	177	2 S54778	NR-13 protein - qu
40	82.5	7.5	255	2 JC7567	cardamoyl-phosphat
41	82.5	7.5	1105	2 S76557	transcription regu
42	82	7.5	300	2 AC1088	syngomyacin synth
43	82	7.5	9376	2 T14593	3-deoxy-D-manno-oc
44	81.5	7.4	416	2 E87286	probable membrane
45	81	7.4	591	2 T44868	

## ALIGNMENTS

## RESULT 1

I53744 gene bcl-2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999

C:Accession: I53744

R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.

Gene 140, 291-292, 1994

A>Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.

A:Reference number: I53744; M0ID:94193015; PMID:8144041

A:Accession: I53744

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236 <RES>

A:Cross-References: GB:L14680; NID:9408946; PIDN:AA53662.1; PID:9408947

A:Gene: bcl-2

C:Superfamily: bcl transforming protein

Query Match 15.0%; Score 164.5; DB 2; Length 236;

Best Local Similarity 23.3%; Pred. No. 1.4e-07;

Matches 52; Conservative 35; Mismatches 79; Indels 57; Gaps 8;

QY	28	VAQAKALG-----REYVHARLRRLAGLSW-----SAPPRASAPG-----	61
DB	1	MAQAGRTGYNREIVAKYIHKLSQKGYEMDGDDEDSAPLRAPPTGIFSFQFESNRTPA	60
QY	62	-----GRLAEVCTVLRRLGDELEQIRPSVYRNVAR-----QLHI-P	96
DB	61	VHRDTAARTSPRLPLVANAGPALSPVPVYHLTLRRAGDDFSRRRRDFAEMSSQLHLTP	120
QY	97	LOSEPVVTDALFVAGHIFAGITGWGVSLYSAAAGLAVDCYRQAPPAVHVLVDCIGE	156
DB	121	FTLR---GREATVELEFLDGVNMGRIVAFFEEGGVCGSVNREMSPLVDNALMTE	176
QY	157	FVKATLTLRRRGQTDVLRKV-VSTPKPGFRHML-VATICS	197
DB	177	YLNRLHLTWIQDNGMDAFVFLXGPSMRPLFDFSWLSIKTLIS	219

## RESULT 2

JC7383 B-cell lymphoma 2 protein - Chinese hamster

C:Species: Cricetus griseus (Chinese hamster)

C>Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 08-Dec-2000

C:Accession: JC7383

R:Tomicic, M.T.; Christmann, M.; Kaina, B.

Biochem. Biophys. Res. Commun. 275, 899-903, 2000

A>Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.

A:Reference number: JC7383

A:Contents: Ovary

A:Accession: JC7383

A: Molecule type: mRNA  
A: Residues: 1-236 <TOM>  
A: Cross-references: GB:AJ271720  
C: Comment: This protein has anti-apoptotic function, and supports cell survival.  
C: Genetics:  
A: Gene: bcl-2  
C: Superfamily: bcl transforming protein  
C: Keywords: B-cell Lymphoma; ovary

Query Match	14.5%	Score 159.5	DB 2	Length 236
Best Local Similarity	22.4%	Pred. No. 4e-07		
Matches 50	Conservative 37	Mismatches 79	Indels 57	Gaps 8

```

Oy 28 VAAQAAALG-----REVHVARLLRAGISW-----SAPESAAPC-----61
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MAQAGRTGYDNRRELYMKYIHKLSRGREYEMDGVDAAPLGAATPGEISFOESNPTPA 60
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Oy 62 -----GRLAEVCYVLLRLGDELEQIRPSYRNVAR-----OLHI-P 96
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 VHRDMAATISPLRPIVATTTGPTLSPPVPPVYHLTLRAGDDFSRRYRRDPAMSSQHLTP 120
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Oy 97 LQSEPVYTDALAVAGHIFSGITGWKAVSLYSAAGLAVDCYRQAPAMVHALVDPCLGE 156
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 121 FTAR-----GREATVEELFRDGVNMGRIVAFEEFGYGVCAVESVREMSPLVDINALMTE 176
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Oy 157 FVRKTIATVLRRRGGWMDYVLCV-VSTRKPGSRHWL-VATLCS 197
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 177 YLNRHLHTWIODNGMDAENAEVLLYSPVSRPLPDRFSWLSLTKTLIS 219
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

RESULT 3  
167432  
bcl-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_Revision 26-Jul-1996 #text-change 16-Jul-1999  
C:Accession: 167432  
R:Tilly, J.L.; Tilly, K.L.; Kenton, M.L.; Johnson, A.L.  
E:Endocodon 136, 233-241, 1995  
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.

Query Match	14.58%	Score	159;	DB	2;	Length	236;
Best Local Similarity	21.58%	Pred	No.	4,	4e-07;		
Matches	51;	Conservative	37;	Mismatches	83;	Indels	66;
						Gaps	8

```

QY 28 VAAKAAAL-----REYHARLLRAGISW-----SAPEASAPG-----61
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MAAGRGTCYDNKRELYMKYIHKLSRGCEYMDTGDEDSAPLRRAFTPGIFSPESNTPA 60
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 62 -----GRLAEVCYVLLRLGDELOIRPSVYRNVAR-----QLHI-P 96
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 VHRDTAARTSPLRLPLVANAGPALSPVPVPHVLLTLRAGDDESRRTYRDDFAEMSSQLHTLP 120
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 97 LQSEPVYVDALVAGHFFSGITGWKVSILYSAAAGLANDCVAAQAPAMVHALVDCGE 156
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 121 FTAR-----GRATAVEELFPDGVNMWGRIVAFEEFGVGVESVREMYPLVDNIALMTE 176
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 157 FVRKTLATLRRRGWMDVLCV--VSTRKPGRSHW-----LVATLQSPGREL 202
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 177 YLNRRLHATWIDNGGMAFVLYLGPSPNMPLPDRFSWQSLKTLTLSTALYAGACTTGCAYTL 233
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 4  
JE0203  
Apoptosis regulator bcl-x isoform - human  
N;Alternate names: h-bcl-xbeta

C:Species: Homo sapiens (man)  
C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 16-Jul-1999  
C:Accession: JE0203  
R:Ban, J.; Echhart, L.; Wengler, W.; Milder, M.; Tschachner, E.  
Biochem. Biophys. Res. Commun. 248, 147-152, 1998  
A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.  
A:Reference number: JE0203; MID:9834085; PMID:9675101

Query Match	14.4%	Score 158.5	DB 2	Length 227
Best Local Similarity	23.5%	Pred. No. 4.7e-07		
Matches 50	Conservative 29	Mismatches 77	Indels 57	Gaps 6

```

OY      23 TDKELVAAKALGGRYVIAALLRGLMS-----APEKA-----56
Dd      4 SNRELIV-----DLSYKLSQKGYMSQSDYDENFTAPEGETESEMEPPSAINGNPS 56
OY      57 -----SPAGGR-----LAEYCVTLRLGDELEQIRPSYVRNAROLHPL 97
Dd      57 WHLADSPAVNGATCHSSSLDAREVIPMAAVKQALREAGDELFELRYRAFSLDTSLQHL-- 114
OY      98 QSEPVYDIAFLAVYAGHIFPSAGITGKVVSLYSAAAGLAVDCVRAOAPMAHALVDCGEF 157
Dd      115 -TPGTAYSQFOYVNNELFRDGVNNGRIYAFPSFGALCVESVDKEMOVLVSRIAMANATY 173
OY      158 VRKTLATWLRRRGM--TDVLKCVYSTRKPGFRS 188
Dd      174 LNDHLEPWIQENGWVRKTKPLVCFFSLASGORS 206

```

RESULT 5  
TVMSAI  
transforming protein bcl-2-alpha - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1998 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999  
C:Accession: A25960; E37532  
R:Negrini, M.; Siliini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.  
Cell 49, 455-463, 1987  
A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho  
A:Reference number: A90893; MUID:87187643; PMID:3032455  
A:Accession: A25960  
A:Molecule type: DNA  
A:Residues: 1-236 <NEC>  
A:Cross-references: GB:J1532; GB:M16506; NID:g468336; PIDN:AA37282.1; PID:g387109  
R:Enrich, Y.; Ewert, D.L.; Tsujimoto, Y.  
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a var  
A:Reference number: A37332; MUID:92375724; PMID:1508712

QY 28 VQAQKALG-----REYVHARLLRAGLSW-----SAPERSAPAG----- 61

Db 1 MAQAGRTGYDNREIVMYKIIHYKISQRYGEMDAGDADADAPLGAAPTPGTFISFDQESNPMA 60

5



A:Map position: 18q21.3-18q21.3

C:Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match

Best Local Similarity 14.0%; Score 153.5; DB 1; Length 239;

Matches 46; Conservative 37; Mismatches 74; Indels 53; Gaps 7;

QY 37 EYVHARLLRAGLSW-----SAPERASAPAG-----GRLAEVCT-- 69

DB 17 KYIHXYLSQRYEMDAGVCAAPGAPAGGIRISQPGHTPHPAASNDPARKSPLOTPTA 76

QY 70 -----VLRGLDELEQIRSVYRNARQOLHI-PLQSEPVYTDALFLA 109

DB 77 APCAAGAPALSPVPVYVHLTLRQAGDDFSRRYRDRFAEMSSQLHLPFTAR---GREAT 132

QY 110 VAGHIFAGITGKVVSLYSAAGLAVDCYRQAPAMVHALVDCLEGFVKTLATMLRR 169

DB 133 VVEELFROGVNMGRIYAFEEFGVCMCVESYRNEMSPLYVDNIATMTETYLNRHLHTWIQDN 192

QY 170 GGWTDVLCV-VSTKPGFRSHML-VATLCS 197

DB 193 GGWDAFVELYCPMRPLDFPFSWLSKTLTS 222

RESULT 9

S24390

Transforming protein (Bcl-2) homolog - chicken

C:Species: Gallus gallus (chicken)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999

C:Accession: S24390

R:Casals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.

Biochim. Biophys. Acta 1132, 109-113, 1992

A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue

A:Reference number: S24390; MUID:92379084; PMID:1511008

A:Accession: S24390

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-232 <CAZ>

A:Cross-references: EMBL:Z11961; NID:962969; PIDN:CAA78018.1; PID:962970

C:Superfamily: bcl transforming protein

C:Keywords: mitochondrion; transmembrane protein

Query Match 13.8%; Score 151.5; DB 2; Length 232;

Best Local Similarity 20.4%; Pred. No. 2.1e-06;

Matches 44; Conservative 36; Mismatches 83; Indels 53; Gaps 5;

QY 37 EYVHARLLRAGLSWSA-----PERASAPAGRLAEVCT----- 69

DB 17 KYIHXYLSQRYEMDAGVCAAPGAPAGGIRISQPGHTPHPAASNDPARKSPLOTPTA 76

QY 70 -----VLRGLDELEQIRSVYRNARQOLHIPLQSEPVYTDALFLAVAGHIFSA 117

DB 77 LRGAAPGCVHLLRQAGDEFSRRYRDRFAEMSSQLHLPFTAR---GREAT 133

QY 118 GTTWKVVSLYSAAGLAVDCYRQAPAMVHALVDCLEGFVKTLATMLRRGGWTDVLC 177

DB 134 GVNWRIYAFEEFGVCMCVESYRNEMSPLYVDNIATMTETYLNRHLHTWIQDN 193

QY 178 CV-VSTKPGFRSHW-----LVATLCSGFRPL 202

DB 194 LVGNSMRPLDFPFSWLSKTLTSVLVGCITIGATL 229

RESULT 10

TVMSB1

transforming protein bcl-2-beta - mouse

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: B25960

R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: B25960

A:Molecule type: DNA

A:Residues: 1-199 <NEG>

A:Cross-references: GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:9387110

C:Genetics:

A:Gene: BCL2

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; transforming protein

Query Match 13.7%; Score 150.5; DB 1; Length 199;

Best Local Similarity 22.1%; Pred. No. 2.2e-06;

Matches 45; Conservative 34; Mismatches 68; Indels 57; Gaps 7;

QY 28 VAQAKALG-----REYHARLLRAGLSW-----SAPERASAPAG----- 61

DB 1 MAQAGRTGYNREIVAKYIKLSQRYEMDADADADAPLGAAPTFGIFSPQESNMPMA 60

QY 62 -----GRLAEVCTVLRGLDELEQIRSVYRNAR-----QLHI-P 96

DB 61 VREMAARTSPRLPLVATAGPALSPPVPCVHLTLRRAGDDFSRRYRDRFAEMSSQLHLP 120

QY 97 LQSEPVYTDALFLAVAGHIFAGITGKVVSLYSAAGLAVDCYRQAPAMVHALVDCLEGF 156

DB 121 FTAR---GREATVVEELFROGVNMGRIYAFEEFGVCMCVESYRNEMSPLYVDNIATMTET 176

QY 157 EVRKTATWLRRRGGWTDVLCV 180

DB 177 YLNRHLHTWIQDNCGW-VGACLV 198

RESULT 11

I49057

bcl-x transmembrane deleted - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I49057

R:Rang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.

J. Immunol. 153, 4388-4398, 1994

A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes

A:Reference number: I49055; MUID:95052604; PMID:7963517

A:Accession: I49057

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-214 <RES>

A:Cross-references: EMBL:U10102; NID:9506649; PIDN:AAA82174.1; PID:9506650

C:Genetics:

A:Gene: bcl-x-long

C:Superfamily: bcl transforming protein

Query Match 13.7%; Score 150.5; DB 2; Length 214;

Best Local Similarity 22.1%; Pred. No. 2.4e-06;

Matches 43; Conservative 29; Mismatches 68; Indels 55; Gaps 5;

QY 23 TRKELVAQKALGREYHARLLRAGLSWS-----APERA----- 56

DB 4 SNRELIV-----DPLSYLSQKGYMSQFSDEENRTAEDETEAERETPSAINGPS 56

QY 57 -----SPARGGR-----LAECVTLRLGDELEQIRSVYRNARQOLHPL 97

DB 57 WHLAQSPVANGATGSHSSIDAREVLPMAVVKQALREAGDEFELRRARRASDLSQHL-- 114

QY 98 QSEPVYTDALFLAVAGHIFAGITGKVVSLYSAAGLAVDCYRQAPAMVHALVDCLEGF 157

DB 115 -TPGTAYQSFQGVNVELEFDGVNMGRIYAFEEFGALCVESDKENQVLYSRIASMATY 173

QY 158 VKRTLATWLRRRGW 172

DB 174 LNDHLEPWIQENGW 188





GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:16:46 : Search time 32.5339 Seconds  
(without alignments)  
872.393 Million cell updates/sec

Title: US-09-682-667-6  
Perfect score: 1100  
Sequence: 1 MEVLRRSSVFPAEIMDAFDR.....TLCSEGRFLKAPFLLPER 213

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_101002:\*

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2: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1981.DAT:\*  
3: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1982.DAT:\*  
4: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1983.DAT:\*  
5: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1984.DAT:\*  
6: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1985.DAT:\*  
7: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1986.DAT:\*  
8: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1987.DAT:\*  
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19: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA1998.DAT:\*  
20: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA2000.DAT:\*  
21: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA2000.DAT:\*  
22: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata/geneeq/geneeqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	100.0	213	20 AAY14155	Human Bcl-2 protein
2	1076	97.8	213	20 AAY14153	Rat Bcl-2 protein se
3	1055	95.9	213	21 AAB41444	Human ORF1208
4	852.5	77.5	170	20 AAY14156	Human Bcl-2 protein
5	821.5	74.7	170	20 AAY14154	Rat Bcl-2 protein se
6	716	65.1	176	21 AAB58949	Breast and ovarian
7	660	60.0	134	22 AAB85665	Human Bcl-2-like p
8	240.5	21.9	846	22 ABB64401	Drosophila melanog
9	230	20.9	247	22 ABB63760	Drosophila melanog
10	159.5	14.5	239	22 AAB48288	Human BCL-2 protei

11	159.5	14.5	239	22 AAB50537	Human Bcl-2 protei
12	158	14.4	232	17 AAM01020	Apoptosis-blocking
13	158	14.4	232	20 AAW94347	Human Bcl-2 mutant
14	157.5	14.3	236	20 AAM07811	A murine Bcl-2 pro
15	157.5	14.3	236	22 AAB74128	Murine Bcl-2. Mus
16	157.5	14.3	236	22 AAB35131	Murine Bcl-2. Mus
17	157.5	14.3	236	23 AAG76554	Murine Bcl-2 polyp
18	157.5	14.3	239	22 AAG64037	Human Bcl-2 protei
19	156.5	14.2	272	17 AAY21120	Human Bcl2 proto-o
20	155.5	14.1	239	17 AAM02383	Human BCL2. Homo
21	155.5	14.1	239	22 AAG64036	Human Bcl-2 protei
22	155.5	14.1	239	22 AAG64038	Human Bcl-2 protei
23	155	14.1	235	19 AAM48312	Mouse Bcl-x gamma.
24	155	14.1	239	21 AAG69203	Amino acid sequenc
25	155	14.1	485	22 AAV00222	LEF-Bcl-XL apopto
26	154.5	14.0	239	9 AAB80987	Sequence of bcl-2-
27	154.5	14.0	239	14 AAR42312	Bcl-2 oncogene pro
28	154.5	14.0	239	16 AAR70331	Human bcl-2 protei
29	154.5	14.0	239	16 AAR71404	Human bcl-2 alpha
30	154.5	14.0	239	17 AAM01018	Apoptosis-blocking
31	154.5	14.0	239	19 AAM40217	Human bcl-2. Homo
32	154.5	14.0	239	20 AAM94345	Human Bcl-2. Homo
33	154.5	14.0	239	20 AAM87812	A human Bcl-2-alph
34	154.5	14.0	239	22 AAE08573	Human Bcl-2 protei
35	154.5	14.0	239	22 AAG64035	Human Bcl-2 protei
36	154.5	14.0	239	22 AAB74129	Human bcl-2alpha.
37	154.5	14.0	239	23 AAB75986	Protein sequence.
38	154.5	14.0	239	23 ABB05227	Human D3A. caspase
39	153.5	14.0	239	20 AAM87810	A human Bcl-2 prot
40	153.5	14.0	239	22 AAB74127	Human Bcl-2. Homo
41	153.5	14.0	239	22 AAB35130	Human Bcl-2. Homo
42	153.5	14.0	239	23 AAV76553	Human Bcl-2 polype
43	152.5	13.9	229	17 AAM01021	Apoptosis-blocking
44	152.5	13.9	229	20 AAM94348	Human Bcl-2 mutant
45	152.5	13.9	239	22 AAG64039	Human Bcl-2 protei

## ALIGNMENTS

RESULT 1  
AAV14155  
ID AAV14155 standard; Protein; 213 AA.  
XX  
AC AAY14155;  
XX  
DT 27-JUL-1999 (first entry)  
XX  
DE Human Bcl-2 protein sequence.  
XX  
Bcl-2-related ovarian killer; BHL1 variant; endometriosis;  
Bcl-2-related ovarian killer; BHL1 variant; endometriosis;  
pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
ovarian carcinoma; granulosa epithelial carcinoma; cancer; therapy;  
proliferative disorder; human.  
XX  
OS Homo sapiens.  
XX  
PN WO9924453-A1.  
XX  
PD 20-MAY-1999.  
XX  
PF 04-NOV-1998; 98WO-US23523.  
XX  
PR 07-NOV-1997; 97US-0064943.  
XX  
(STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
PA Hsu SY, Hsueh AWJ;  
XX  
PI WPI: 1999-327356/27.  
XX  
DR N-PSDB; AAX61105.  
XX

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
PT protein and its related gene

PS Claim 2; Page 55-56; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.

XX Sequence 213 AA:

SO Query Match 100.0%; Score 1100; DB 20; Length 213;  
Best Local Similarity 100.0%; Pred. No. 3.6e-112;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDARDRPTDKELYAQAALGREYVHARLLRAGLSMSAPERASAP 60  
DB 1 MEVLRSSVFPAEIMDARDRPTDKELYAQAALGREYVHARLLRAGLSMSAPERASAP 60  
OY 61 GGRLAEEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120  
DB 61 GGRLAEEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120  
OY 121 WGVVSLYSAAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
DB 121 WGVVSLYSAAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
OY 181 STKPGFRSHMLVATLCSFGRFKAAPFLLPPER 213  
DB 181 STKPGFRSHMLVATLCSFGRFKAAPFLLPPER 213

RESULT 2  
ID AAY14153 standard; Protein: 213 AA.  
AAY14153

XX AAY14153;

DT 27-JUL-1999 (first entry)

XX Rat Bok protein sequence.

DE Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
KW proliferative disorder; rat.

XX Rattus rattus.

XX MO9924453-A1.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US35323.

XX 07-NOV-1997; 97US-0064943.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Hsu SY, Hsueh AJW;

XX WPI: 1999-327356/27.

DR N-PSDB; AAX61103.

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
PT protein and its related gene

PS Claim 2; Page 53-54; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.

XX Sequence 213 AA:

SO Query Match 97.8%; Score 1076; DB 20; Length 213;  
Best Local Similarity 98.6%; Pred. No. 1.5e-109;  
Matches 210; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDARDRPTDKELYAQAALGREYVHARLLRAGLSMSAPERASAP 60  
DB 1 MEVLRSSVFPAEIMDARDRPTDKELYAQAALGREYVHARLLRAGLSMSAPERASAP 60  
OY 61 GGRLAEEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120  
DB 61 GGRLAEEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120  
OY 121 WGVVSLYSAAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
DB 121 WGVVSLYSAAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
OY 181 STKPGFRSHMLVATLCSFGRFKAAPFLLPPER 213  
DB 181 STKPGFRSHMLVATLCSFGRFKAAPFLLPPER 213

RESULT 3  
ID AAB41444 standard; Protein: 213 AA.  
AAB41444

XX AAB41444;

DT 08-FEB-2001 (first entry)

XX Human OREF1208 polypeptide sequence SEQ ID NO:2416.

DE Human; open reading frame; OREF; detection; cytosolic; hepatotropic;  
KW vulnerability; antiparkinsonian; neurotropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antithematic; antithyroid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;



KW		cholesterol ester storage; systemic lupus erythematosus; infection;
KV		severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM		allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KX		bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW		thrombosis; contraceptive.
XX		
OS		Homo sapiens.
PN		MO200058473-A2.
PN		
PD		05-OCT-2000.
XX		
PF		31-MAR-2000; 2000WO-US08621.
XX		
PR		31-MAR-1999; 99US-0127607.
PR		02-APR-1999; 99US-0127636.
PR		05-APR-1999; 99US-0127728.
XX		30-MAR-2000; 2000US-0540763.
XX		
PA		(CURA-) CURAGEN CORP.
PI		Shimkets RA, Leach M;
DR		WPI: 2000-602362/57.
DR		N-PSDB; AAC75653.
PT		
PT		Noval nucleic acids and peptides derived from open reading frame X,
XX		useful for treating e.g. cancers, proliferative disorders,
XX		neurodegenerative disorders and cardiovascular disease -
PS		Claim 11; Page 1750-1751; 5507pp; English.
XX		
CC	AAC74446	to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC		which represent the human OREX open reading frames 1 to 3161. The OREX
CC		sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC		antiproliferative; antiparkinsonian; nootropic; neuroprotective;
CC		osteopathic; anticoagulant; antiarrhythmic; immunosuppressant;
CC		immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC		antidiabetic; hypotensive; dermatological; immunosuppressive;
CC		antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC		antithyroid; and antihaemic. The sequences can be used for determining
CC		the presence of or predisposition to, or preventing or treating
CC		pathological conditions associated with an OREX-associated disorder. Th
CC		nucleic acids can be used to express OREX proteins in gene therapy
CC		vectors. The proteins and nucleic acids may be used to treat cancers,
CC		proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC		graft vs host disease, cardiovascular disease, diabetes mellitus,
CC		hypertransfusion, hypothyroidism, cholesterol ester storage, systemic lupus
CC		erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC		bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC		allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC		nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC		coagulation; to inhibit thrombosis; and as a contraceptive.
XX		
SQ	Sequence	213 AA;
	Query Match	95.9%; Score 1055; DB 21; Length 213;
	Best Local Similarity	95.8%; Pred. No. 3.1e-107;
	Matches 204; Conservative	2; Mismatches 7; Indels 0; Gaps
OY	1 MEVRRSSVFSAEIMDAFDMPTDKELVAQAQKALGREYVHARLRAGLSMSAPERASAP	60
Db	1 MEVRRSSVFSAEIMDAFDMPTDKELVAQAQKALGREYVHARLRAGLSMSAPERASAP	60
OY	61 GGRLAEVCVTYLRLGDELFOIRPSVYRVANVAQLHIPLQSEPVYTDALFLAVAGHIFSAGIT	120
Db	61 GGRLAEVCVTYLRLGDELFOIRPSVYRVANVAQLHIPLQSEPVYTDALFLAVAGHIFSAGIT	120
OY	121 MGKVYSLYTSAAGAIVPCDVOAOAPAMVAHALVDGCGEFFRKRLATMLRLRGSGMTVLKCV	180
Db	121 MGKVYSLYTSAAGAIVPCDVOAOAPAMVAHALVDGCGEFFRKRLATMLRLRGSGMTVLKCV	180
OY	181 STRGFNSHWLVATLCSFGRLKAAPFLLLPER	213

[illegible]

DB 61 GGRLAEEVCTVLLRL-----GIT 77  
QY 121 MCKVSVLSAAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRRGWTDLKCV 180  
DB 78 MCKVSVLSAAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRRGWTDLKCV 137  
QY 181 STKPGFRSHMLVATLCSFGFRFLKAAFFLLPPER 213  
DB 138 STKPGFRSHMLVATLCSFGFRFLKAAFFLLPPER 170  
RESULT 5  
AAV14154  
ID AAV14154 standard; Protein; 170 AA.  
AC AAV14154;  
XX 27-JUL-1999 (first entry)  
DT 27-JUL-1999 (first entry)  
DE Rat Bok protein sequence.  
XX Bok protein; Bcl-2-related ovarian killer; BH31 variant; endometriosis;  
XX pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
XX reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
XX ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
XX proliferative disorder; rat.  
XX Rattus rattus.  
XX OS  
XX PN WO9924453-A1.  
XX 20-MAY-1999.  
XX 04-NOV-1998; 98WO-US23523.  
XX PF 07-NOV-1997; 97US-0064943.  
XX PR (STRD) UNIV LELAND STANFORD JUNIOR.  
XX PA  
XX Hsu SY, Hsueh ATW;  
XX WPI; 1999-327356/27.  
XX DR N-PSDB; AAX61104.  
XX PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
XX protein and its related gene  
PS Claim 2; Page 54-55; 62pp; English.  
XX  
XX This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
XX protein, of the invention. Coding sequences for Bok or BH31 variants of  
XX pro-apoptotic Bok-related protein can be introduced into cell populations  
XX to upregulate expression of the proteins in order to induce apoptosis in  
XX the cell population. This is useful for treatment of diseases where there  
XX is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
XX and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
XX carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
XX by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
XX protein can be used to elucidate apoptosis mechanisms in reproductive and  
XX other tissues, and provide a means for manipulating apoptosis. The Bok  
XX protein and transgenic animal are also useful for identifying ligands or  
XX substrates. Modulation of the gene activity in vivo is useful for  
XX prophylaxis and therapy of, e.g. cancer and other proliferative  
XX disorders. Bok genes are also useful for identification of cell type  
XX based on expression. Identification of Bok as a new pro-apoptotic protein  
XX with wide tissue distribution and heterodimerisation properties  
XX facilitates elucidation of apoptosis mechanisms.  
SQ Sequence 170 AA;  
Query Match 74.7%; Score 821.5; DB 20; Length 170;  
Best Local Similarity 77.9%; Pred. No. 8.5e-82;  
Matches 166; Conservative 0; Mismatches 4; Indels 43; Gaps 1;

QY 1 MEVLRSSVFAAEIMDAFDPMTDKELVAQAKALGREYHARILRAGLSWSAPERASPAP 60  
DB 1 MEVLRSSVFAAEIMDAFDPMTDKELVAQAKALGREYHARILRAGLSWSAPERASPAP 60  
QY 61 GGRLAEEVCTVLLRLGDELEQIRPSYRNVAROLHLPLOSEPVYTAFLAVAGHISAGIT 120  
DB 61 GGRLAEEVCTVLLRL-----GIT 77  
QY 121 MCKVSVLSAAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRRGWTDLKCV 180  
DB 78 MCKVSVLSAAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRRGWTDLKCV 137  
QY 181 STKPGFRSHMLVATLCSFGFRFLKAAFFLLPPER 213  
DB 138 STKPGFRSHMLVATLCSFGFRFLKAAFFLLPPER 170  
RESULT 6  
AAB58949  
ID AAB58949 standard; Protein; 176 AA.  
AC AAB58949;  
XX 27-MAR-2001 (first entry)  
DT 27-MAR-2001 (first entry)  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.  
XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
XX neotropic; neuroprotective; antiviral; antiatherogenic; hepatotropic;  
XX antidiabetic; antinflammatory; anticancer; vulnerary; anticonvulsant;  
XX antibacterial; antifungal; antiparasitic; cardiac; immune disorder;  
XX Addison's disease; allergy; autoimmune haemolytic anaemia;  
XX autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
XX multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
XX cardiovascular disorder; wound healing; neurological disease.  
XX KW  
XX OS Homo sapiens.  
XX PN WO20005173-A1.  
XX 21-SEP-2000.  
XX PD 08-MAR-2000; 2000WO-US05881.  
XX PF 12-MAR-1999; 99US-0124270.  
XX PR (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX Rosen CA, Ruben SM;  
XX WPI; 2000-611515/58.  
XX DR N-PSDB; AAF21852.  
XX PT New human breast and ovarian cancer associated gene sequences and the  
XX polypeptides encoded by these genes, useful in the prevention,  
XX treatment and diagnosis of cancer, immune disorders, cardiovascular  
XX disorders and neurological diseases -  
PS Claim 11; Page 1103; 1299pp; English.  
XX  
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are  
XX associated with breast and ovarian cancer. Included in the invention are  
XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
XX isolation and characterisation of the DNA and protein sequences of the  
XX invention. The breast and ovarian cancer associated DNA, protein, agonist  
XX or antagonist sequences exhibit cytostatic; immunosuppressive;  
XX neotropic; neuroprotective; antiviral; antiatherogenic; hepatotropic;  
XX antidiabetic; antinflammatory; anticancer; vulnerary; anticonvulsant;  
XX antibacterial; antifungal; antiparasitic and cardiac activity. The  
XX polynucleotide and protein sequences are used in the diagnosis of cancer,  
XX particularly breast and ovarian cancer. The nucleic acid sequences,



(ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 846 AA;  
Query Match 21.9%; Score 240.5; DB 22; Length 846;  
Best Local Similarity 35.3%; Pred. No. 2.8e-17;  
Matches 55; Conservative 27; Mismatches 65; Indels 9; Gaps 4;  
QY 26 ELVAQAKALGREYVHARLLRAG--LSMSAPER-----ASPARGRLEAVCTVLLRLGDELQ 80  
DB 96 DIIINGKCLGQYIRARLRKAGVLRNKYTORLRNIIIDPESSVHVVEFPALSMGEELE 155  
QY 81 IRPSYRVNAROL-HIP--LQSEPVYTDAPLAVAGHIFSAGITGKVSLXSAAAGLAV 136  
DB 156 MHPRYTNTSRLSRAPEGELESDMAPRLNLVAKDLFRSSITGKIIISIFAVCGGFAL 215  
QY 137 DCVROAQAPAMVHALVDCIGEFYRKTATLWLRRCGW 172  
DB 216 DCVROGHEDYLOCLIDGLAEIIEDLVYWLINGGW 251  
RESULT 9  
ABB63760  
ID ABB63760 standard; Protein: 247 AA.  
XX  
AC ABB63760;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 18072.  
XX  
KM Drosophila; developmental biology; cell signalling; insecticide;  
XX pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PE 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
XX  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
XX  
DR N-PSDB; ABL07863.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Disclosure; SEQ ID NO 18072; 21pp + sequence listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

SQ Sequence 247 AA;  
Query Match 20.9%; Score 230; DB 22; Length 247;  
Best Local Similarity 33.3%; Pred. No. 8.2e-17;  
Matches 54; Conservative 28; Mismatches 62; Indels 18; Gaps 4;  
QY 25 KELVAQAKALGREYVHARLLRAGL--SMSAPERASPARC---GRLEAVCTVLLRLGDEL 78  
DB 87 ODIIISGRCICGHYIKRRLRSGLFNKKLGIRISIIIGSTSMGIVRVFPVAVGLGDEL 146  
QY 79 EDIRPSYRVNAROL-----HIPLOSEPVYTDAPLAVAGHIFSAGITGKVSLXS 130  
DB 147 ERMHPRITNGVARQICRNDGGEFHTP---DAVSLLGAVGRELFREVLITMSKVISLRAI 202  
QY 131 AAGLAVDCVROAQAPAMVHALVDCIGEFYRKTATLWLRRCGW 172  
DB 203 AGLSVDCVROGHPEFLPRLMESVEVLEDELVPINENGW 244  
RESULT 10  
AAB48288  
ID AAB48288 standard; Protein: 239 AA.  
XX  
AC AAB48288;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human BCL-2 protein.  
XX  
KM S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
KM CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
KM Bad; Bcl-2; tumour; cytosolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200075184-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 05-JUN-2000; 2000WO-US15449.  
XX  
PR 04-JUN-1999; 99US-0137494.  
XX  
PA (UYIA ) UNIV YALE.  
XX  
PI Zhang H, Tsvetkov IM, Kondo T;  
XX WPI; 2001-061703/07.  
XX  
DR N-PSDB; AAC84600.  
XX  
PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
PT involves altering levels of proteins such as S-phase kinase associated  
PT proteins 1, 2 and cullin/CDC53 proteins -  
XX  
PS Claim 5; Page 104-108; 162pp; English.  
XX  
CC The invention relates to methods of altering the polypeptide levels in a  
CC cell, using proteins selected from S-phase kinase associated proteins 1  
CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
CC cullin/CDC53 family of proteins). The method is useful for altering the  
CC level of p27 cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
CC that modulate interactions between SKP and target proteins are useful for  
CC treating tumours.  
XX  
SQ Sequence 239 AA;  
Query Match 14.5%; Score 159.5; DB 22; Length 239;  
Best Local Similarity 22.4%; Pred. No. 4.1e-09;  
Matches 47; Conservative 37; Mismatches 73; Indels 53; Gaps 7;  
QY 37 EYVHARLLRAGLSW-----SAPERASPARC-----GRLEAVCT-- 69



D<sub>b</sub> 133 DGVMMGRVAFEEEGCVCESVNREMSPLVDNALMTEYLNRHLLHTWTDNGGDFAFV 1922  
Q<sub>y</sub> 177 KCV-VSTKPGFRSHWL-VATICS 197  
          :     | : | |     | : | | |  
D<sub>b</sub> 193 ELVGSRMRPLEDFSMLSIKTILS 215

## RESULT 13

AAW94347  
ID AAW94347 standard; Protein; 232 AA.

AAW94347;

DT 13-APR-1999 (first entry)

Human Bcl-2 mutant protein #80-6.

KM Human; N1p1, N1p2, N1p3, B1p1a, B1p5, B1p13; adenovirus; cell death;  
KM viral infection; Bcl-2; protooncogene; mutational analysis; apoptosis;  
KM E1B 19K protein; cell survival regulation.

OS	Homo sapiens.
OS	Synthetic.

PN US5858678-A.

PD 12-JAN-1999.

PF 21-MAR-1995; 95US-0408095.

PR 02-AUG-1994; 94US-0284139.  
31-MAR-1995; 95US-0408005

XX  
BA /HYST - ) TINTY SE IOUTS

XX  
DT  
Chinaseehera C.

XX WPT: 1999-1530  
DP

polymerides that by

PT Polypeptides that bind to anti-apoptotic proteins - useful for  
PT protecting against cell death induced by viral infection and to  
PT modulate response to physical and chemical stimuli

PS Example 8; Column 43-46; 41pp; English

The present invention describes (1) a method for regulating cell death comprising exposing an isolated cell to a polypeptide selected from Nip1, Nip2, Nip3, Bip1a, Bip3 and Bip1; (2) a method for neutralising the activity of the adenovirus E1B 19 kD protein, the Bcl-2 protein or the BHRF-1 protein, comprising exposing an isolated cell to a polypeptide as in (1); and (3) a method for detecting molecules that bind to at least one polypeptide as in (1), comprising lysing cells, exposing the lysate to the polypeptide and detecting any molecule-polypeptide aggregates. The methods are useful for providing proteins able to bind to other proteins known to regulate cell survival e.g. it is known that E1B 19K protein provides a survival function similar to the cellular protooncogene bcl-2 gene product which is able to block apoptosis in haematopoietic B and T cells. The present sequence represents a human Bcl-2 mutant protein from the present invention.

SQ Sequence 232 AA;

Query Match	14.4%;	Score 158;	DB 20;	Length 232;
Best Local Similarity	22.7%;	Pred. No. 5.8e-09;		
Matches 46;	Conservative 37;	Mismatches 74;	Indels 46;	Gaps 7;

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0Y      37 EYVHARLRAGLSW-----SAPERASPACG-----GRAEVCT--69
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Oy 70 -----VLLRLGDELEQIRPSVRYRNARQQLHT-PLQSEPVVTDFAVLAVAGHIFS 116
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 77 APGSPVPVYHLTLRQAGDESRRYRRDFAEMSSQHLHLPFTAR----GCFATVVEELFR 132Z

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Oy 117 AGITNGKVSLSYLSAAGIAYDVCVQAOAPAMNHALVYDLDGEFVRRTATYTLRRSGMFDYL 176
    | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 133 DGVNMGRIVAEFFEGGVCSESVARENSPLVDNIALMTEYLNNHLLHTWILQDNGMFAFV 192

Oy 177 KCV-VSTKGFGRSHML-VATLCS 197
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 193 ELYGSPMRPLDFEFSWLKTLILS 215
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 14

ID	AAW87811	standard; Protein; 236 AA
xx		

AC AAW87811;

DT 10-MAR-1999 (first entry)  
 YY

DE A murine Bcl-2 protein.

KM Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;  
KW bcl-2-related function; apoptosis; dimer; Bcl-xL; Mcl-1; AL.

OS	Mus sp.
xy	

PN US5856171-A.  
xx

05-JAN-1999

PF 10-NOV-1994; 94DS-0337646.  
XX

PR	10-NOV-1994;	94US-0337646.
PR	36-AUG-1993;	93US-0113308.

PR 25-MAY-1994; 9405-0248819-  
XX

PA (UNIT) UNIV WASHINGTON.  
XX  
XX

Pl korsimeyer su;  
xx

DR WFL: 1999-103119/09  
XX

PT DNA composition encodes identifying modulators

PT Identifying modulators of bcl-2 function  
 XX  
 PS Example 10; Fig 7; 105pp; English.  
 YY

The present sequence represents a specification also describes PC-1

CC designated Bax. The Bax protein is used in a composition which  
CC comprises a bcl-2 family member polypeptide, a naturally occurring  
CC Bax polypeptide and an antibody that binds to the Bax polypeptide.  
CC The specification also describes a composition comprising a hybrid  
CC protein comprising an activator domain of a transcriptional activator  
CC protein and a bcl-2 family member having a BH1 domain and a BH2 domain;  
CC another hybrid protein comprising a DNA-binding domain of the  
CC transcriptional activator protein and a second bcl-2 family member  
CC having a BH1 domain and a BH2 domain; and a reporter gene linked to a  
CC transcriptional regulatory element whose transcriptional activity is  
CC dependent on the presence or absence of a dimer of the two hybrid  
CC proteins. The bcl-2 family members are selected from naturally occurring  
CC Bcl-2, Bcl-XL, Bax, Mcl-1, A1, fragments thereof, and mutants having a  
CC mutation in the BH1 and/or BH2 domain that alters intermolecular binding  
CC of the two bcl-2 family members. The compositions are used to identify  
CC modulators of bcl-2-related function, e.g. substances that inhibit  
CC binding of Bax to bcl-2, which would be potentially useful as drugs  
CC for modulating apoptosis.

SQ	Sequence	236 AA;
----	----------	---------

Query Match	14.3%	Score 157.5	DB 20	Length 236
Best Local Similarity	22.4%	Pred. No. 6.8e-09		
Matches 50	Conservative 37	Mismatches 79	Indels 57	Gaps 8

```

OY 28 VAOAKALG-----REYVHARLLRAGLSW-----SAPERASPAQC-----61
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MAQAGRTGYNREIVMKYIHKLSQRCYENDAGDADAPLGAAPTPTGIFSFQESNMPA 60
OY 62 -----GRLAECTVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 VHRMMAARTSPRLPLVATAGPALSPVPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120
OY 97 LOSEPVTDAFLVAGHIFSGITGKRVSLYSAAAGLAVDCYRQAPAVHALLVDCLGE 156
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 121 FTAR-----GRFATVVEELFRDGVNMGRIVAFEEFGVCMCVESVNRKSPLYDNIALMTE 176
OY 157 EVAKTLATWLRRRGWTDVLKCV-VSTKPGFRSHWL-VATLCS 197
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 177 YLNRHLHTWTIQDNGWDAPFVELYGPMSMRPLDFDSWLSLTKTLLS 219

RESULT 15
AAB74128
ID AAB74128 standard; Protein; 236 AA.
XX
AC AAB74128;
XX
DT 22-MAY-2001 (first entry)
XX
DE Murine bcl-2.
XX
KW Murine; Bax; cytostatic; immunosuppressive; immunostimulant; infection;
KW apoptosis modulator; bcl-2 associated x protein; cancer therapy; AIDS;
KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
KW myocardial infarction; traumatic brain injury; ischemia; bcl-2;
KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
KW lymphoproliferative disease.
XX
OS Mus sp.
XX
PN US6184202-B1.
XX
PD 06-FEB-2001.
XX
PF 11-SEP-1997; 97US-0927326.
XX
PR 10-NOV-1994; 94US-0337646.
PR 26-AUG-1993; 93US-0112208.
PR 25-MAY-1994; 94US-0248619.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 2001-256104/26.
XX
PT Modulating apoptosis of a cell, useful in maintaining homeostasis in
PT adult tissues, or treating proliferative or autoimmune diseases,
PT comprises administering a bcl-2 polypeptide that interacts with a 21 kd
PT bcl-2 associated x protein
XX
PS Example 7; Fig 7; 105pp; English.
XX
CC The present invention relates to a method of modulating apoptosis of a
CC cell. The method comprises administering to the cell an agent,
CC comprising a Bhl domain or BH2 domain, capable of modulating formation of
CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
CC complexes, bcl-2 associated x protein (Bax):Bax complexes, bcl-2:Bax
CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
CC traumatic brain injury, neurodegenerative diseases, aging, ischemia,
CC toxemia, infection, hepatitis, transplant rejection, and
CC lymphoproliferative diseases. The present sequence is murine Bcl-2, which
CC was used in a sequence alignment in the present invention, with murine
CC Bax (AAB74125), human Bax (AAB74126) and human Bcl-2 (AAB74127).
XX

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SQ Sequence 236 AA;
Query Match 14.3%; Score 157.5; DB 22; Length 236;
Best Local Similarity 22.4%; Pred. No. 6.8e-09;
Matches 50; Conservative 37; Mismatches 79; Indels 57; Gaps 8;

OY 28 VAOAKALG-----REYVHARLLRAGLSW-----SAPERASPAQC-----61
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MAQAGRTGYNREIVMKYIHKLSQRCYENDAGDADAPLGAAPTPTGIFSFQESNMPA 60
OY 62 -----GRLAECTVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 VHRMMAARTSPRLPLVATAGPALSPVPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120
OY 97 LOSEPVTDAFLVAGHIFSGITGKRVSLYSAAAGLAVDCYRQAPAVHALLVDCLGE 156
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 121 FTAR-----GRFATVVEELFRDGVNMGRIVAFEEFGVCMCVESVNRKSPLYDNIALMTE 176
OY 157 EVAKTLATWLRRRGWTDVLKCV-VSTKPGFRSHWL-VATLCS 197
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 177 YLNRHLHTWTIQDNGWDAPFVELYGPMSMRPLDFDSWLSLTKTLLS 219

Search completed: April 29, 2003, 11:23:23
Job time : 33.5339 secs

```





GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:19:46 ; Search time 21.7493 seconds  
(without alignments)  
1610.532 Million cell updates/sec

Title: US-09-682-667-8  
Perfect score: 884  
Sequence: 1 MEVLRRSSVFYFAEIMDAFDR.....TLCSPGFLKAFLLPER 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	860	97.3	170	11 088857	088857 rattus norv
2	852.5	96.4	213	4 09UJ32	09UJ32 homo sapien
3	828.5	93.7	213	11 035425	035425 rattus norv
4	783	88.6	212	4 09UWX3	09UWX3 homo sapien
5	681.5	77.1	213	13 091812	091812 gallus gall
6	675.5	76.4	213	13 09DGJ5	09dgj5 gallus gall
7	178	20.1	299	5 08RXY5	08rxy5 drosophila
8	178	20.1	313	5 09NGX3	09ngx3 drosophila
9	169.5	19.2	247	5 09VG12	09vg12 drosophila
10	169	19.1	300	5 09V9C8	09v9c8 drosophila
11	138	15.6	317	5 09S083	09s083 drosophila
12	129.5	14.6	236	11 0923R6	0923r6 cricetus
13	108.5	12.3	192	13 0919N4	0919n4 brachydanio
14	108.5	12.3	219	11 099N36	099n36 mus musculu
15	108.5	12.3	235	11 035843	035843 mus musculu
16	107.5	12.2	233	11 035844	035844 mus musculu

17	106.5	12.0	238	13 090298	090298 brachydanio
18	104.5	11.8	233	6 08SO42	08so42 felis silve
19	104	11.8	188	11 09QWX2	09qwx2 mus musculu
20	104	11.8	217	11 099N35	099n35 mus musculu
21	103	11.7	180	6 09BDS7	09bds7 bos taurus
22	103	11.7	233	6 09MZS7	09mzs7 ovis aries
23	103	11.7	233	6 09N1A2	09n1a2 sus scrofa
24	102	11.5	188	4 09H1R6	09h1r6 homo sapien
25	102	11.5	233	6 09MYW4	09myw4 oryctolagus
26	101	11.4	180	6 09BDX7	09bdx7 bos taurus
27	99	11.2	193	11 08B996	08b996 rattus norv
28	99	11.2	221	13 09B013	09b013 xenopus lae
29	98.5	11.1	163	6 09MZS6	09mzs6 ovis aries
30	98	11.1	204	13 0902H2	0902h2 xenopus lae
31	97	11.0	178	11 09CYW5	09cyw5 mus musculu
32	97	11.0	179	4 09NNG7	09nng7 homo sapien
33	94	10.6	173	11 090KL3	090kl3 rattus norv
34	93	10.5	172	11 055177	055177 mus musculu
35	92	10.4	114	4 09NR76	09nr76 homo sapien
36	92	10.4	149	6 09CMG7	09cmg7 ovis aries
37	92	10.4	173	4 08WZ49	08wz49 homo sapien
38	92	10.4	192	6 08S043	08s043 felis silve
39	90	10.2	209	11 090K59	090k59 rattus norv
40	89.5	10.1	172	11 055179	055179 mus musculu
41	86	9.7	2497	16 08XYB9	08xyb9 raietonia s
42	85	9.6	175	11 0925A9	0925a9 rattus norv
43	85	9.6	177	2 09AEZ3	09aez3 frankia sp
44	85	9.6	185	12 08YBG1	08ybg1 hepatitis b
45	84.5	9.6	182	16 08XUQ3	08xuq3 raietonia s

## ALIGNMENTS

## RESULT 1

ID 088857 PRELIMINARY; PRT; 170 AA.

AC 088857;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Bcl-2-related ovarian killer protein.  
GN BOK.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-OVARY;  
RX MEDLINE-98024143; PubMed-9356461;  
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
RT "Bok is a pro-apoptotic bcl-2 protein with restricted expression in  
reproductive tissues and heterodimerizes with selective anti-apoptotic  
bcl-2 family members.";  
RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-OVARY;  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "A splicing variant of the Bcl-2 member Bok with a truncated BH3  
domain induces apoptosis without dimerization with anti-apoptotic Bcl-  
2 proteins.";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF051093; AAC61928.1; -;  
DR InterPro: IPR000712; Bcl2.BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL; 1.  
DR PROSITE: PSS0062; BCL2\_FAMILY; 1.  
SQ SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

Query Match 97.3% Score 860; DB 11; Length 170;

Best Local Similarity 96.2%; Pred. No. 4,5e-72;  
Matches 167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60  
DB 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60  
QY 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLA 120  
DB 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLA 120  
QY 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCGFRFLKAAFFLLPER 170  
DB 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCGFRFLKAAFFLLPER 170

RESULT 2  
09UL32 PRELIMINARY; PRT: 213 AA.

AC 09UL32;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Bcl-2 related ovarian killer.  
GN BOK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "CDNA cloning of the human BOK gene."  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF089746; AAF09129.1;  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; Bcl2\_family.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL; 1.  
DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
DR SEQUENCE 213 AA; 23540 MW; 59509F8C730517F CRC64;

Query Match 96.4%; Score 852.5; DB 4; Length 213;  
Best Local Similarity 79.8%; Pred. No. 2.9e-71;  
Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60  
DB 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60  
QY 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLA 120  
DB 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLA 120  
QY 78 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLATWLRGGMTDVLKCV 137  
DB 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLATWLRGGMTDVLKCV 180  
QY 138 STKPGFRSHMLVATLCGFRFLKAAFFLLPER 170  
DB 181 STKPGFRSHMLVATLCGFRFLKAAFFLLPER 213

RESULT 3  
035425 PRELIMINARY; PRT: 213 AA.

AC 035425;  
DT 01-JAN-1998 (Tremblrel. 05, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE BCL-2-related ovarian killer protein.  
GN BOK OR BOKL OR BOK OR MTD.  
OS Rattus norvegicus (Rat), and

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116, 10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat; STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, AND UTERUS;  
RX MEDLINE=98024143; PubMed=9356461;  
RA Hsu S.Y., Kaipia A., McGee E., Iomeli M., Hsueh A.J.W.;  
RT "BOK is a pro-apoptotic Bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic Bcl-2 family members."  
RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat; STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, AND UTERUS;  
RA Hsu S.Y., Hsueh A.J.W.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Mouse;  
RA Inohara N., Ekheraee D., Garcia I., Carrio R., Merino J., Merry A., Chen S., Nunez G.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF027707; AAC53582.1;  
DR MGD; MGI:1858494; BOK.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; Bcl2\_family.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL; 1.  
DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
DR SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

Query Match 93.7%; Score 828.5; DB 11; Length 213;  
Best Local Similarity 78.4%; Pred. No. 4.8e-69;  
Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

QY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60  
DB 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60  
QY 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLA 120  
DB 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLA 120  
QY 78 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLATWLRGGMTDVLKCV 137  
DB 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFYRKTLLATWLRGGMTDVLKCV 180  
QY 138 STKPGFRSHMLVATLCGFRFLKAAFFLLPER 170  
DB 181 STKPGFRSHMLVATLCGFRFLKAAFFLLPER 213

RESULT 4  
09UMX3 PRELIMINARY; PRT: 212 AA.

AC 09UMX3;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE BCL-2-related ovarian killer protein (Similar to BCL-2-related ovarian killer protein-like-PENDING) (BCL-2-related ovarian killer protein-like).  
GN BOK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang H.;

"Gene expression of a human homolog of BCL-2-related ovarian killer

protein.";

RT Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.

RC SEQUENCE FROM N.A.

RP TISSUE-MUSCLE;

RA Strausberg R.;

RU Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

RC TISSUE-MUSCLE;

RA Strausberg R.;

RU Submitted (Nov-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF174487; AAD51719.1; -

DR EMBL: BC006203; AAH06203.1; -

DR EMBL: BC017214; AAH17214.1; -

DR InterPro: IPR000712; BCL2\_Fam.

DR Pfam: PF00452; BCL-2; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

Matches 131; Conservative 18; Mismatches 21; Indels 43; Gaps 1;

QY 1 MEYLRRSSVFAAEIMAFDPMPTDKELVAQAKLGREYVHARLLRAGLSASAPERASAP 60

DB 1 MEYLRRSSVFAAEVMEVDFRSPDKELVSAQAKLGRDINSRLIRAGVSKREHNPVP 60

QY 61 GGRLAECVTLRL-----GTF 77

DB 61 GGRLAECVTLRL-----GTF 77

QY 78 WGRVSLYSAAAGLAVDCVQAQAPAMVHALVDCLGEFVRKTLATWLRRCGWTDLKCV 137

DB 121 WGRVSLYSAAAGLAVDCVQAQAPAMVHALVDCLGEFVRKTLATWLRRCGWTDLKCV 180

QY 138 STPKGFRSHLVATLCSFGRLKAFFLLPER 170

DB 181 STPKGFRSHLVATLCSFGRLKAFFLLPER 213

RESULT 6

Q9DGJ5 PRELIMINARY; PRT; 213 AA.

AC Q9DGJ5

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Bcl-2-related ovarian killer protein.

OS Gallus gallus (Chicken).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

SEQUENCE FROM N.A.

RA Mills E.M., Johnson A.L., Bridgman J.T.;

RT "Characterization and Expression of Bcl-2 in the Hen Ovary."

RU Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF290888; AAG01182.1; -

DR InterPro: IPR000712; BCL2\_Fam.

DR Pfam: PF00452; BCL-2; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

Matches 129; Conservative 19; Mismatches 22; Indels 43; Gaps 1;

QY 1 MEYLRRSSVFAAEIMAFDPMPTDKELVAQAKLGREYVHARLLRAGLSASAPERASAP 60

DB 1 MEYLRRSSVFAAEVMEVDFRSPDKELVSAQAKLGRDINSRLIRAGVSKREHNPVP 60

QY 61 GGRLAECVTLRL-----GTF 77

DB 61 GGRLAECVTLRL-----GTF 77

QY 78 WGRVSLYSAAAGLAVDCVQAQAPAMVHALVDCLGEFVRKTLATWLRRCGWTDLKCV 137

DB 121 WGRVSLYSAAAGLAVDCVQAQAPAMVHALVDCLGEFVRKTLATWLRRCGWTDLKCV 180

QY 138 STPKGFRSHLVATLCSFGRLKAFFLLPER 170

DB 181 STPKGFRSHLVATLCSFGRLKAFFLLPER 213

RESULT 7

Q8TR8Y PRELIMINARY; PRT; 299 AA.

AC Q8TR8Y

DT 01-JUN-2002 (Tremblrel. 21, Created)

DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Bcl-2-related ovarian killer protein.

OS Gallus gallus (Chicken).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

SEQUENCE FROM N.A.

RA Zhang H., Holzgreve W., De Geyter C.;

RT "Evolutionarily conserved Bcl-2 family."

RU Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF275944; AAF81282.1; -

DR InterPro: IPR000712; BCL2\_Fam.

DR Pfam: PF00452; BCL-2; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DE ARI6536P.  
 GN BUFLY.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 OX NCBI [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Abbayani A., Carlson J.,  
 RA Champ M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Patagas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY075219; AAL68086.1; -  
 SO SEQUENCE 299 AA; 33379 MW; 7FB125A6B7323B23 CRC64;

Query Match 20.1%, Score 178; DB 5; Length 299;  
 Best Local Similarity 26.9%, Pred. No. 1.2e-08;  
 Matches 56; Conservative 24; Mismatches 62; Indels 66; Gaps 8;

OY 25 KEVVAQAKALREYVHARLRAGL-----SNAP----- 53  
 DB 87 QDIIISQGRCLGCHYIKRRLRSRGLKGLQIRISLIGSTSMGIVRDVFPVAVYLDEL 146  
 OY 54 ERASPA-----PGGR-----LAEVCTVLRIGITMGKVVSLYSAAAGL 91  
 DB 147 ERMHRIINGVARQICRNPGGFEHFPDVAISLLGAVNGRELFPVETWKSIVSLFPAAGL 206  
 OY 92 AVDCVRQAOPAMVHALVDCLGFEVFKTLATWLRRRGW---TDVLCVCVSTKPGFRSHW 147  
 DB 207 SVDCVRQCHPEYLPKLMESVSEVIEDLVPMINENGWGSINTHVLPTTNSLNP---LEW 263  
 OY 148 LVATL-CSFG-----RLKAAFFILLPE 169  
 DB 264 TTLVIGVVFGLLVFMILRFITLIVPK 291

RESULT 8  
 O9NGX3 PRELIMINARY; PRT; 313 AA.  
 AC O9NGX3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bcl-2-like protein BUFLY (Fragment).  
 GN BUFLY OR CG8238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 OX NCBI [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=2013510; PubMed=10684252;  
 RA Colussi P.A., Quinn L.M., Huang D.C., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RT "Debel, a proapoptotic bcl-2 homologue, is a component of the  
 RT Drosophila melanogaster cell death machinery."  
 RL J. Cell Biol. 148:703-714(2000).  
 DR EMBL: AF237864; AAF44120.1; -;  
 DR HSPB; Q07817; IMA2.  
 DR Flybase; FBgn0040491; BUFLY.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
 DR NON TER 1  
 SO SEQUENCE 313 AA; 34909 MW; 775A1FDD5B678E CRC64;

Query Match 20.1%, Score 178; DB 5; Length 313;  
 Best Local Similarity 26.9%, Pred. No. 1.2e-08;  
 Matches 56; Conservative 24; Mismatches 62; Indels 66; Gaps 8;  
 OY 25 KEVVAQAKALREYVHARLRAGL-----SNAP----- 53  
 DB 101 QDIIISQGRCLGCHYIKRRLRSRGLKGLQIRISLIGSTSMGIVRDVFPVAVYLDEL 160  
 OY 54 ERASPA-----PGGR-----LAEVCTVLRIGITMGKVVSLYSAAAGL 91  
 DB 161 ERMHRIINGVARQICRNPGGFEHFPDVAISLLGAVNGRELFPVETWKSIVSLFPAAGL 220  
 OY 92 AVDCVRQAOPAMVHALVDCLGFEVFKTLATWLRRRGW---TDVLCVCVSTKPGFRSHW 147  
 DB 221 SVDCVRQCHPEYLPKLMESVSEVIEDLVPMINENGWGSINTHVLPTTNSLNP---LEW 277  
 OY 148 LVATL-CSFG-----RLKAAFFILLPE 169  
 DB 278 TTLVIGVVFGLLVFMILRFITLIVPK 305

RESULT 9  
 O9V612 PRELIMINARY; PRT; 247 AA.  
 AC O9V612;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE CG8238 protein.  
 GN BUFLY OR CG8238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 OX NCBI [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champ M., Pfeiffer B.D.,  
 RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalaia M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon R., Nuskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003825; AAF58628.1; -.  
 DR HSSP: Q07817; IMAZ.  
 DR FlyBase: FBgn0040491; Buflf.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR Pfam: PF00452; Bcl-2.1.  
 DR SMART: SM00337; BCL1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR SEQUENCE 247 AA: 27466 MW: A204325AF64C1620 CRC64:  
 SQ  
 Query Match 19.2%; Score 169.5; DB 5; Length 247;  
 Best Local Similarity 27.8%; Pred. No. 5.8e-08;  
 Matches 44; Conservative 19; Mismatches 42; Indels 53; Gaps 4;  
 OY 25 KELVAQAKALGREGVYHARLLRAGL-----SWSAP----- 53  
 DB 87 ODLSQGRCLCGHYIKRRLRSGLFKLQIRISILGSTSGMGIADVFPAYQVLGDEL 146  
 OY 54 ERASRA-----PGGR-----LAECYVLRLGLTGKVSISXAAGL 91  
 DB 147 ERMHPRITNGVARQICRNPGGEPHPDPAVSLLLGAVGRELFREYETWVSISLFAIAGL 206  
 OY 92 AVDCVRAQAPAMVHALVDCLEGFEVKTATWLRRCGW 129  
 DB 207 SYDCVRQGHPEYLPKIMESVSEVIDELVPMINENGW 244  
 RESULT 10  
 OY9VC8 PRELIMINARY: PRT: 300 AA.  
 AC OY9VC8:  
 DT 01-MAR-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Death EXECUTIONER Bcl-2 homolog protein (PROAPOPTOTIC BCL-2 homolog  
 DE DEBEL) (BCL-2 family member protein) (BCL-2 ORTHOLOG DBORG-1).  
 GN DEBEL OR DBORG1 OR BOK OR BCL2 OR ROB-1 OR CG123397.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-EMBRIO;  
 RA MEDLINE=20105529; PubMed=2015529;  
 RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Nunez G., Okano H.,  
 RA Miura M.;  
 RT "Drob-1, a *Drosophila* member of the Bcl-2/CED-9 family that promotes  
 RT cell death.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:662-667(2000).  
 RN [2]  
 RP REVISIONS TO N-TERMINUS.  
 RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Okano H., Miura M.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=2015310; PubMed=10684252;  
 RA Colussi P.A., Quinn L.M., Huang D.C.S., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RT "Debel, a proapoptotic Bcl-2 homologue, is a component of the  
 RT *Drosophila melanogaster* cell death machinery.";  
 RL J. Cell Biol. 148:703-714(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Zhang H., Huang Q., Ke N., Matsuyama S., Hammock B., Godzik A.,  
 RA Reed J.C.;  
 RT "Drosophila pro-apoptotic Bcl-2/Bax homolog reveals evolutionary  
 RT conservation of cell death mechanisms.";

RL J. Biol. Chem. 0:0-0(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton R.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Brottaker P.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durkin K.J., Evangelista C.C., Ferraz C., Fertlira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merulov G., Mishina N.V., Modarri C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock D.A., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Kurada P., White K.;  
 RT "Putative *Drosophila* homolog of mammalian Bcl-2-related ovarian killer  
 RT protein.";  
 RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Zhou L., Steller H.;  
 RT "Potential *Drosophila* homologue of Bcl-2-related ovarian killer  
 RT (BOK).";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Brachmann C.B., Jassim O.W., Wachsmuth B.D., Cagan R.L.;  
 RT "dborg-1, a *Drosophila* Bcl-2 family member that functions in the  
 RT apoptotic response to UV-irradiation.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA EMBL: AB032430; BAA89603.2; -.  
 DR EMBL: AF149798; AAF26841.1; ALT\_INIT.  
 DR EMBL: AF178430; AAF26289.1; -.  
 DR EMBL: AF228044; AAF89165.1; -.  
 DR EMBL: AE003789; AAF57365.1; ALT\_TERM.  
 DR EMBL: AF216752; AAF25955.1; ALT\_TERM.  
 DR EMBL: AF222004; AAF44324.1; -.  
 DR EMBL: AF244352; AAF44714.1; -.  
 DR FlyBase: FBgn0029131; debcl.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; BCL2\_FAMILY.  
 DR InterPro: IPR000822; Znf\_C2H2.

DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW DNA-binding; zinc-finger.  
 FT CONFLICT 1 86 MISSING (IN REF. 4).  
 FT CONFLICT 215 215 I -> V (IN REF. 1).  
 FT CONFLICT 217 217 C -> R (IN REF. 4).  
 SQ SEQUENCE 300 AA; 32940 MM; FE29E0ADC3D0942 CRC64;

Query Match 19.1%; Score 169; DB 5; Length 300;  
 Best Local Similarity 27.6%; Pred. No. 8e-08;  
 Matches 43; Conservative 17; Mismatches 44; Indels 52; Gaps 3;

QY 26 ELVAQAALGREGYHARLRAG-LSWSAPER----- 55  
 DB 96 DIINGKCLCGOYIRARLRAGVLRNRYQRLRLDPGSSHYVEVPALNSMGEELR 155  
 QY 56 -----ASAPGGRLAE-----VCTVLRIGITGWKVVSLXSAAGLAV 93  
 DB 156 MHPVYTNISRLSRAPGELSDMAPMLNLVAKDLFRSSITWGKITSIFAVCGGFAT 215  
 QY 94 DCVROAQPAMVHALVDCGFEFVRKTLATWLRRCGM 129  
 DB 216 DCVROGHFDYLOCLIDGLAEITIEDLVYWLIDNGM 251

## RESULT 11

Q95U83 PRELIMINARY; PRT; 317 AA.

ID 095U83  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GH01265P.  
 GN DEBL OR CG12397.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN NCBI  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farlan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY058249; AAL13478.1; -;  
 DR FLYBase: FBgn0029131; debcl.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 SQ SEQUENCE 317 AA; 34649 MM; 46B22FED1CC6F01F CRC64;

Query Match 15.6%; Score 138; DB 5; Length 317;  
 Best Local Similarity 26.8%; Pred. No. 6.3e-05;  
 Matches 42; Conservative 18; Mismatches 43; Indels 54; Gaps 4;

QY 26 ELVAQAALGREGYHARLRAG-LSWSAPER----- 55  
 DB 96 DIINGKCLCGOYIRARLRAGVLRNRYQRLRLDPGSSHYVEVPALNSMGEELR 155  
 QY 56 -----ASAPGGRLAE-----VCTVLRIGITGWKVVSLXSAAGLAV 93  
 DB 156 MHPVYTNISRLSRAPGELSDMAPMLNLVAKDLFRSSITWGKITSIFAVCGGFAT 215  
 QY 94 DCVROAQPAMVHALVDCGFEFVRK-TLATWLRRCGM 128  
 DB 216 DCVROGHFDYLOCLIDGLAEITIGRGLADRQRWVG 252

## RESULT 12

Q923R6 PRELIMINARY; PRT; 236 AA.

ID 0923R6  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B-cell lymphoma protein 2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Rodentia; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
 NCBI\_TaxID=10030;  
 RN NCBI  
 RP SEQUENCE FROM N.A.  
 RA Lai D.Z., Chen W., Wang H.T.;  
 RT "Construction of a robust CHO cell line for biopharmaceutical use."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF404339; AAK92201.1; -;  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR InterPro: IPR004723; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR TIGRfams: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
 DR PROSITE: PS01259; BH3; UNKNOWN\_1.  
 DR PROSITE: PS01260; BH4\_1; UNKNOWN\_1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 SQ SEQUENCE 236 AA; 26500 MM; BEDF052EF32CA8B8 CRC64;

Query Match 14.6%; Score 129.5; DB 11; Length 236;  
 Best Local Similarity 18.9%; Pred. No. 0.00026;  
 Matches 40; Conservative 26; Mismatches 55; Indels 91; Gaps 4;

QY 28 VQAQKALG-----REYVHARLRAGLSW-----SAPERASPARG----- 61  
 DB 1 MAQAGRTGYDNRRELYMKIYHKLSGRYGEMDGVDAAPLGAAPYGFISQPSNPRA 60  
 QY 62 ----- 61  
 DB 61 VHRDMAARTSPLRPVATTTGPTLSPVPPVHLTLRRAGDDFSRRYRDFAEWSSQLHLTP 120  
 QY 62 -----GLAEVCTVLRIGITGWKVVSLXSAAGLAVDCVROAQPAMVHALVDCGFEFVRK 117  
 DB 121 FTARGFATVVEELFRDGVNMGRIVAFFEGGVNCSVNRMSPLVDNIALMTEYLNR 180  
 QY 118 TLATWLRRCGMVDLKCIV-VSTKPGFRSHWL 148  
 DB 181 HLHTWIDONGMDAFVELYXGVSRLPFDPSWL 212

## RESULT 13

Q919N4 PRELIMINARY; PRT; 192 AA.

ID 0919N4  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bax.  
 GN BAX.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Teleostei; Osteichthyes; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN NCBI  
 RP SEQUENCE FROM N.A.

RX MEDLINE-20373792; PubMed-10917738;  
 RA Inohara N., Nunez G.;  
 RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
 RU Cell Death Differ. 7:509-510(2000).  
 DR EMBL; AF231015; AAF66960.1; -.  
 DR HSSP; P53563; IAF3.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 192 AA; 21401 MW; 8A71A630A56FDC32 CRC64;

Query Match 12.3%; Score 108.5; DB 13; Length 192;  
 Best Local Similarity 21.0%; Pred. No. 0.019; Mismatches 64; Indels 35; Gaps 4;  
 Matches 34; Conservative 29;

OY 6 RSSVFAEIMDAFDRWPTDELVAQAKALGREYVHARLLRAGLSWSAPERASAPGRLA 65  
 DB 45 RSLGGVELCD-----PSHKRLAQCIQIGDELGDGNAQSLN-----NSNQ 88  
 OY 66 EYCTVLLRGIITWGVSLYSAAGLAVDCVROQAPAMVHALVDCIGFEVVK 117  
 DB 89 PQQDFIRVAREIFSDGKFNMGVVALFACRLVYKAISTRVPIIRTIISWTMSYIOE 148  
 OY 118 TLATVLRGRGWTDLVKCVSTRKPGFRSHWLVAATLCSFGRL 159  
 DB 149 HYINMIREQGM-----DGIIRSYFGTPTMOTVAVFL 179

RESULT 14  
 O99N36 PRELIMINARY; PRT; 219 AA.  
 AC O99N36;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B-cell leukemia/lymphoma x-gamma (Fragment).  
 GN BCLX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129/SVT;  
 RA Yang X.-F., Cantor H.;  
 RT "Novel cDNA structure and genomic organization of apoptosis regulatory gene Bcl-x-gamma."  
 RT Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF133279; AAK15454.1; -.  
 DR EMBL; AF133281; AAK15454.1; JOINED.  
 DR HSSP; P53563; IAF3.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 219 AA; 24224 MW; EB352EC4CFAA6AF5 CRC64;

Query Match 12.3%; Score 108.5; DB 11; Length 219;  
 Best Local Similarity 23.0%; Pred. No. 0.022; Mismatches 43; Indels 15; Gaps 3;  
 Matches 25; Conservative 17;

OY 66 EYCTVLLRGIITWGVSLYSAAGLAVDCVROQAPAMVHALVDCIGFEVVK 125  
 DB 109 QVYNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLSRIASMAATYLNHLEPWIDE 168  
 OY 126 RGGW-----TDVLKCVVSTKPGFRSH-----WLVAAT 151

DB 169 NGMGVSGGTPLRVFRRLVQV-PGVAEHVCDPSLMEVET 207

RESULT 15  
 O35843 PRELIMINARY; PRT; 235 AA.  
 AC O35843;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bcl-x-gamma.  
 GN BCL2L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B6/CBA; TISSUE-THYMUS;  
 RX MEDLINE-98051053; PubMed-9390687;  
 RA Yang X.-F., Weber G.F., Cantor H.;  
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells."  
 RT Immunity 7:629-639(1997).  
 RL EMBL; U51277; AAC53458.1; -.  
 DR HSSP; P53563; IAF3.  
 DR MGD; MGI:88139; Bcl2L.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR004725; BCL2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR TIGRPFAMS; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;

Query Match 12.3%; Score 108.5; DB 11; Length 235;  
 Best Local Similarity 25.0%; Pred. No. 0.024; Mismatches 43; Indels 15; Gaps 3;  
 Matches 25; Conservative 17;

OY 66 EYCTVLLRGIITWGVSLYSAAGLAVDCVROQAPAMVHALVDCIGFEVVK 125  
 DB 125 QVYNELFRDGVNMGRIVAFPSFGALCVESVDKEMQVLSRIASMAATYLNHLEPWIDE 184  
 OY 126 RGGW-----TDVLKCVVSTKPGFRSH-----WLVAAT 151  
 DB 185 NGMGVSGGTPLRVFRRLVQV-PGVAEHVCDPSLMEVET 223

Search completed: April 29, 2003, 11:25:41  
 Job time : 22.7493 secs





GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 5.99217 Seconds  
(without alignments)  
1176.699 Million cell updates/sec

Title: US-09-682-667-8  
Perfect score: 884  
Sequence: 1 MEVLRRSSVFPAEIMDAFDR.....TLCSEGRFLKAFFLLPER 170

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	140	15.8	236 1	BCL2_RAT
2	133	15.0	239 1	BCL2_HUMAN
3	132	14.9	229 1	BCL2_BOVIN
4	131	14.8	236 1	BCL2_CRIO
5	130	14.7	236 1	BCL2_MOUSE
6	115.5	13.1	233 1	BCL2_CHICK
7	112.5	12.7	228 1	ARL_XENLA
8	104.5	11.8	229 1	BCLX_CHICK
9	104	11.8	233 1	BCLX_MOUSE
10	103	11.8	233 1	BCLX_RAT
11	103	11.7	233 1	BCLX_PIG
12	102	11.5	233 1	BCLX_HUMAN
13	100	11.3	218 1	BAXX_HUMAN
14	99	11.2	193 1	BCLW_MOUSE
15	98	11.1	204 1	ARL1_XENLA
16	95	10.7	192 1	BAXXA_HUMAN
17	95	10.7	193 1	BCLW_HUMAN
18	95	10.7	211 1	BAK_HUMAN
19	94	10.6	192 1	BAXXA_MOUSE
20	94	10.6	192 1	BAKX_RAT
21	92.5	10.5	143 1	BAKX_HUMAN
22	92	10.4	192 1	BAXXA_BOVIN
23	90	10.2	208 1	BAK_MOUSE
24	85.5	9.7	172 1	BEL1_MOUSE
25	85	9.6	211 1	BAK2_HUMAN
26	84	9.5	535 1	SSDH_HUMAN
27	83	9.4	1115 1	CARB_MYCTU
28	81	9.2	416 1	CHRA_PSEAE
29	77.5	8.8	2291 1	SPCB_DROME
30	77	8.7	175 1	BEL1_HUMAN
31	76.5	8.7	2128 1	SPCB_MOUSE
32	76	8.6	185 1	CORA_HPBW
33	76	8.6	212 1	CORA_HPBW

34	76	8.6	370 1	ID12_PYRAB	Q9uzs9 pyrococcus
35	76	8.6	1300 1	IRR_MOUSE	O9wt14 mus musculu
36	75.5	8.5	1121 1	CARB_MOUSE	O9ccr2 mycobacteri
37	75.5	8.5	2564 1	SPCO_HUMAN	O9t254 homo sapien
38	75	8.5	401 1	PLIC_PSEPU	P36641 homo sapien
39	74.5	8.4	516 1	YAKT_RHISN	P55538 rhizobium s
40	74	8.4	185 1	CORA_HPBW2	P03148 hepatitis b
41	74	8.4	297 1	NADC_HUMAN	O15274 homo sapien
42	74	8.4	2137 1	SPCB_HUMAN	P11277 homo sapien
43	73.5	8.3	378 1	YH12_MYCTU	Q10400 mycobacteri
44	73.5	8.3	539 1	TCP2_CAEBL	P46550 caenorhabdi
45	73.5	8.3	610 1	RHO_MYCLE	P45835 mycobacteri

## ALIGNMENTS

RESULT 1  
BCL2\_RAT STANDARD: PRT; 236 AA.  
AC P49950: 062837: 064032:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2 OR BCL-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94193015; PubMed=8144041;  
RA Sato T., Irie S., Krajewski S., Reed J.C.;  
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";  
RL Gene 140:291-292(1994).  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
RX MEDLINE=95129487; PubMed=7828536;  
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
RT "Expression of members of the bcl-2 gene family in the immature rat  
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
cell apoptosis is associated with decreased bax and constitutive  
bcl-2 and bcl-xl-long messenger ribonucleic acid levels.";  
RL Endocrinology 136:232-241(1995).  
[3]  
RN SEQUENCE OF 19-172 FROM N.A.  
RX MEDLINE=95059917; PubMed=7969891;  
RA Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,  
RA Lindholm D.;  
RT "bcl-2 messenger RNA is localized in neurons of the developing and  
adult rat brain.";  
RL Neuroscience 61:165-177(1994).  
-i- FUNCTION: Suppresses apoptosis in a variety of cell systems  
including factor-dependent lymphohematopoietic and neural cells.  
Regulates cell death by controlling the mitochondrial membrane  
permeability. Appears to function in a feedback loop system with  
caspases. Inhibits caspase activity either by preventing the  
release of cytochrome c from the mitochondria and/or by binding to  
the apoptosis-activating factor (APAF-1).  
-i- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
Bcl-xL. Heterodimerization with BAX requires intact BH1 and BH2  
domains, and is necessary for anti-apoptotic activity (by  
similarity). Also interacts with APAF-1 and RAIF-1 (by similarity).  
-i- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
membrane of the nuclear envelope and the endoplasmic reticulum.  
-i- TISSUE SPECIFICITY: Expressed in a variety of tissues, with  
highest levels in reproductive tissues. In the adult brain,  
expression is localized in mitral cells of the olfactory bulb,  
granule and pyramidal neurons of hippocampus, pontine nuclei,  
cerebellar granule neurons, and in ependymal cells. In prenatal

CC brain, expression is higher and localized in the neuroepithelium  
CC and in the cortical plate.  
CC -1- DOMAIN: The B4 domain is required for anti-apoptotic activity and  
CC for interaction with RAF-1 (By similarity).  
CC -1- PPM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
CC occurs during the G2/M phase of the cell cycle. In the absence of  
CC growth factors, Bcl2 appears to be phosphorylated by other protein  
CC kinases such as ERKs and stress-activated kinases.  
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
CC -1- PPM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the B4 domain, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol  
CC promoting further caspase activity (By similarity).  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U14680; AAA53662.1; -  
DR EMBL: U34964; AAA77687.1; -  
DR EMBL: S74122; -; NOT\_ANNOTATED\_CDS.  
DR HSSP: Q07817; 1MAZ.  
DR InterPro: IPR002475; BCL2\_family.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH.  
DR InterPro: IPR004725; Bcl2\_reg.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART: SM00337; BCL; 1.  
DR SMART: SM00265; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PSS0062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01258; BH2; 1.  
DR PROSITE: PS01259; BH3; 1.  
DR PROSITE: PS01260; BH4\_1; 1.  
DR PROSITE: PSS0063; BH4\_2; 1.  
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
FT DOMAIN 10 30 BH4.  
FT DOMAIN 90 104 BH3.  
FT DOMAIN 133 152 BH1.  
FT DOMAIN 184 199 BH2.  
FT TRANSMEM 209 230  
FT SITE 34 35 POTENTIAL.  
FT MOD\_RES 70 70 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
FT CONFLICT 42 42 A -> R (IN REF. 2).  
FT CONFLICT 157 157 E -> G (IN REF. 1).  
FT CONFLICT 164 164 S -> Y (IN REF. 2).  
FT CONFLICT 212 212 L -> O (IN REF. 2).  
SQ SEQUENCE 236 AA; 26622 MW; E7686CB9071A872A CRC64;  
Query Match 15.8%; Score 140; DB 1; Length 236;  
Best Local Similarity 20.5%; Pred. No. 1.5e-06;  
Matches 45; Conservative 26; Mismatches 56; Indels 92; Gaps 5;  
OY 28 VAQKALG-----REYVARLLRAGISW-----SAPEASAPC----- 61  
DB 1 MAQAGRGYDNRLEVMRYIHKLSRGYEDTGDSDAPLRAAPPGIFSPQPSNRTPA 60  
OY 62 ----- 61  
DB 61 VHRDTARTSPRLPLVANAGPALSPVPVVLTLRRAGDPSRRYRRDFAEMSQLHLP 120

OY 62 -----GRLAEVCTVLLRLGITWGVSYSAAGIAVDCVRQACPAMHATVDCIGFEVRK 117  
DB 121 FTAGRFATVVEELFRGVNMGRIVAFFEGVCVSEVNMSPDIVDNIAIMMTETLNR 180  
OY 118 TLATWLRRRGGTDLKCV-VSTPGRSHWL-VATLCS 154  
DB 181 HLHTWIDONGDAFVELYGPSMRPLDFSWLSIKTLIS 219  
RESULT 2  
BCL2\_HUMAN  
ID BCL2\_HUMAN STANDARD; PRT; 239 AA.  
AC P10415; P10416; Q16197; Q13842;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RX MEDLINE=86259760; PubMed=3523487;  
RA Tsujimoto Y., Croce C.M.;  
RT "Analysis of the structure, transcripts, and protein products of  
RT bcl-2, the gene involved in human follicular lymphoma";  
RT Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).  
RN [2]  
RP REVISTONS TO 96; 110 AND 237.  
RX MEDLINE=92375724; PubMed=1508712;  
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
RT "Isolation and characterization of the chicken bcl-2 gene: expression  
RT in a variety of tissues including lymphoid and neuronal organs in  
RT adult and embryo".  
RL Nucleic Acids Res. 20:4187-4192(1992).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=87002488; PubMed=2875799;  
RA Cleary M.L., Smith S.D., Sklar J.;  
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-  
RT 2/immunoglobulin transcript resulting from the t(14;18)  
RL translocation".  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=88196071; PubMed=2834197;  
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,  
RA Goldman P., Korsmeyer S.J.;  
RT "Alternative promoters and exons, somatic mutation and deregulation  
RT of the Bcl-2-Ig fusion gene in lymphoma".  
RL EMBO J. 7:123-131(1988).  
RN [5]  
RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.  
RX MEDLINE=92096610; PubMed=1339299;  
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;  
RT "Frequent incidence of somatic mutations in translocated BCL2  
RT oncogenes of non-Hodgkin's lymphomas".  
RL Blood 79:229-237(1992).  
RN [6]  
RP SUBCELLULAR LOCATION.  
RX MEDLINE=91066924; PubMed=2250705;  
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;  
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks  
RT programmed cell death".  
RL Nature 348:334-336(1990).  
RN [7]  
RP MUTAGENESIS.  
RX MEDLINE=94239528; PubMed=8183370;  
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;  
RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of



OY 131 DVLCV-VSTRKGRSHWL-VATLCS 154  
 DB 197 AFVELYGPMSRPLDFSWLSKTLIS 222

RESULT 3  
 BCL2\_BOVIN STANDARD; PRT; 229 AA.  
 ID BCL2\_BOVIN  
 AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=Thymus;  
 RA Reyes R.A., Cockrell G.L.;  
 RT "Bovine leukemia virus associated-leukemogenesis is correlated  
 with suppression of programmed cell death and increased expression  
 of Bcl-2."  
 RT Submitted (MAR-1997) to the EMBL/GenBank/DDJ databases.  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 permeability. Appears to function in a feedback loop system with  
 caspases. Inhibits caspase activity either by preventing the  
 release of cytochrome c from the mitochondria and/or by binding to  
 the apoptosis-activating factor (APAF-1) (By similarity).  
 CC SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 domains, and is necessary for anti-apoptotic activity (By  
 similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).  
 CC SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 membrane of the nuclear envelope and the endoplasmic reticulum (By  
 similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 for interaction with RAIF-1 (By similarity).  
 CC -1- PPM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 on Ser-70 by PKC is required for the anti-apoptosis activity and  
 occurs during the G2/M phase of the cell cycle (By similarity). In  
 the absence of growth factors, Bcl2 appears to be phosphorylated  
 by other protein kinases such as ERKs and stress-activated  
 kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
 similarity).  
 CC -1- PPM: Proteolytically cleaved by caspases during apoptosis. The  
 cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 activity, causes the release of cytochrome c into the cytosol  
 promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U92434; AAB53319.1; -  
 CC HSP: Q07817; 1MA2  
 CC InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_Reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfams: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30  
 FT DOMAIN 64 68  
 FT DOMAIN 69 72  
 FT DOMAIN 83 97  
 FT DOMAIN 126 145  
 FT DOMAIN 177 192  
 FT DOMAIN 202 223  
 FT SITE 34 35  
 FT MOD\_RES 63 63  
 SQ SEQUENCE 229 AA; 2509 MW; ADIDDAF98FFIID CRC64;  
 Query Match 14.9%; Score 132; DB 1; Length 229;  
 Best Local Similarity 19.7%; Pred. No. 8.4e-06;  
 Matches 41; Conservative 26; Mismatches 55; Indels 86; Gaps 4;  
 OY 37 EYVARLRRLRSLW-----SAPERASAPG----- 61  
 DB 17 KYIHKLQSRQYEWADGAGAPGAAPGILSSQGRTPAPRTSPPPAAAGAP 76  
 OY 62 -----GRAEYCTVLLRLGITWGK 80  
 DB 77 SPVPYVHLTLRQAGDDPSRRYRDFAEMSQLHTPTTARERATVEELFROGVNMR 136  
 OY 81 VSLYSAAAGLAVDCVROQAPAMVHALVDCGEFVRKTLATWLRRGWDVLCV-VST 139  
 DB 137 IVAFEEFGVCVCSVSNREMSPLVDLSIALMWTETVLRHLHTIWDNGDAFVELYGPSM 196  
 OY 140 KQGRSHWLVAITLCSFGHFLKAAFFLL 167  
 DB 197 RPLDFSWL-----SKALLSLAL 215  
 RESULT 4  
 BCL2\_CRILLO STANDARD; PRT; 236 AA.  
 ID BCL2\_CRILLO  
 AC Q9JUV8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCBI\_TaxID=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=20431763; PubMed=10973819;  
 RA Tomitic M.T., Christmann M., Kaina B.;  
 RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2  
 protein."  
 RT Blochem. Biophys. Res. Commun. 275:899-903(2000).  
 RL [2]  
 RP SEQUENCE FROM N.A.; AND CLEAVAGE BY CASPASES.  
 RX MEDLINE=21092839; PubMed=11101062;  
 RA Tomitic M.T., Kaina B.;



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CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- ALTERATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAf-1.
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL, L31532; AAA37282.1; -.
DR EMBL, M16506; AAA37282.1; JOINED.
DR EMBL, M16506; AAA37281.1; -.
DR PIR, A25960; TVMSA1.
DR PIR, B25960; TVMSB1.
DR PIR, E37332; E37332.
DR HSSP, Q07817; IMAZ.
DR MGD, MGI:88138; Bcl2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_Reg.
DR Pfam, PF00452; Bcl-2; 1.
DR Pfam, PF02180; BH4; 1.
DR SMART, SM00337; BCL; 1.
DR SMART, SM00265; BH4; 1.
DR TIGRFAMs, TIGR00865; bcl-2; 1.
DR PROSITE, PSS0062; BCL2_FAMILY; 1.
DR PROSITE, PS01080; BH1; 1.
DR PROSITE, PS01258; BH2; 1.
DR PROSITE, PS01259; BH3; 1.
DR PROSITE, PS01260; BH4_1; 1.
DR PROSITE, PSS0063; BH4_2; 1.
DR APOPTOSIS: Alternative splicing; Transmembrane; Mitochondrion;
KM Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC).
FT VARSPIC 193 236 DAFVELGPMRPLFDFGSMRLTSLKTLISLVGACITLGVAVL
FT VARSPLIC 193 236 GHK -> VGACTIVE (IN ISOPORM BETA).
SO SEQUENCE 236 AA; 26425 MW; AA85EF6B0766BEDA CRC64;
Query Match 14.78; Score 130; DB 1; Length 236;
Best Local Similarity 19.68; Pred. No. 1,4e-05;
Matches 43; Conservative 27; Mismatches 57; Indels 92; Gaps 5;
OY 28 VQAQKALG-----REYVARLRLRAGLSW-----SAPERASAPAP----- 61

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Db 1 MAQAGRTGYDNRREIVKRYIHYKLSQGYEMDAGDADAPLAAPPGIFSPQSPNPAPA 60
OY 62 ----- 61
Db 61 VIREMAATSPRLPLVATAGPALSPVPCVHLTLRRAGDDPSRRYRDRFAEMSSOLHLP 120
OY 62 -----GRLEAVCTVLLRLGITWGVSLYSAAAGLAVDCVQAQAPMAVHALVDCLEFVRK 117
Db 121 FTAREFAFTVVEELFRDQVMNGRIYAFEEFGVKGCVESVNMESPLVONIALMTEYINR 180
OY 118 TLATLRRRGWTDVLCV-VSTKPFRRSHL-VATLCS 154
Db 181 HLHTWIDQNGMDAFELVGPMSRPLFDFGSMRLTSLKTLIS 219
RESULT 6
BCL2_CHICK STANDARD; PRT; 233 AA.
AC Q00709;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
CN BCL2 OR BCL-2.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo."
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=B-cell lymphoma;
RX MEDLINE=92379084; PubMed=1511008;
RA Cazalis-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
RT Bcl-2."
RL Biochim. Biophys. Acta 1132:109-113(1992).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAf-1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
CC kidney, heart, ovary and brain, with the highest levels in the
CC thymus. In the embryo, highly levels expressed in all tissues with
CC high levels in the bursa of Fabricius.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAf-1 (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----  
DR EMBL; D11382; BAA01978.1; -  
DR EMBL; D11381; BAA01978.1; JOINED.  
DR EMBL; 211961; CAA78018.1; -  
DR PIR; A37332; A37332.  
DR PIR; S24390; S24390.  
DR HSP; Q07817; IMAZ.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR000712; BCL2\_BH.  
DR InterPro; IPR003093; BCL2\_BH4.  
DR InterPro; IPR004725; BCL2\_Reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR Apoptosis; Transmembrane; Mitochondrion.  
KW DOMAIN 10 30 BH4.  
FT DOMAIN 87 101 BH3.  
FT DOMAIN 130 149 BH1.  
FT DOMAIN 181 196 BH2.  
FT TRANSMEM 208 228 POTENTIAL.  
FT CONFLICT 64 64 E -> S (IN REF. 2).  
FT CONFLICT 67 82 GSAASEVPPAEGLRP -> ARLLVRCPLRGCA  
(IN REF. 2).  
FT CONFLICT 121 121 H -> T (IN REF. 2).  
FT CONFLICT 139 139 G -> V (IN REF. 2).  
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6AC3D CRC64;

Query Match 13.1%; Score 115.5; DB 1; Length 233;  
Best Local Similarity 16.4%; Pred. No. 0.00035;  
Matches 33; Conservative 26; Mismatches 62; Indels 91; Gaps 3;

QY 37 EYVHARLRLAGLSWSPAPRAAP----- 60  
DB 17 KYIHKLSQRYDWAAGDRPVPAPAPAAVAAGASSHHRRPPGSAASEVPP 76  
QY 61 -----GRLAECYVLLRLGI 76  
DB 77 AEGLRPAPGVHALLRQAGDEFRRYORDFQMSQGLHLPFTAHGREFVAVEELFRDGV 136  
QY 77 TWGKVSLSYSAAGLAVDCVQAPAMVHALVDLGEFVRKTLATWLRRRGGMTDVKCV 136  
DB 137 NWGRIVAFEEGVCVSVNREMSPLVDNATWTFETLNRHLNHIODNGMDAFLVELY 196  
QY 137 -VSTKPGFRSHM-----LVATLCSFGRFL 159  
DB 197 GNSMRPLDFSMISLTKITLSLVVGACITLGAYL 230

RESULT 7  
ARI\_XENLA  
ID ARI\_XENLA STANDARD; PRT; 228 AA.  
AC 091827;  
DT 01-NOV-1997 (Rel. 35, Last Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator R1 (XRL) (Fragment).  
OS Xenopus laevis (African clawed frog).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head;  
RX MEDLINE=95331613; PubMed=7607538;  
RA Cruz-Reyes J., Tata J.R.;  
RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
cell-survival genes.";  
RL Gene 158:171-179(1995).

CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).  
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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DR EMBL; X82462; CAA57845.1; -  
DR HSP; Q07817; IMAZ.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR000712; BCL2\_BH.  
DR InterPro; IPR003093; BCL2\_BH4.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR Apoptosis; Transmembrane.  
KW DOMAIN 1 1  
FT DOMAIN 120 139 BH1.  
FT DOMAIN 171 186 BH2.  
FT TRANSMEM 207 227 POTENTIAL.  
SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 12.7%; Score 112.5; DB 1; Length 228;  
Best Local Similarity 21.3%; Pred. No. 0.00066;  
Matches 33; Conservative 27; Mismatches 52; Indels 43; Gaps 4;

QY 19 DRWPTDKELVAVQ---AKALGREYVHARLRLAGLSWSPAPRAAP----- 59  
DB 32 DKYLTEGQWMAQSDGSAVLYEDLVRYKLQCSL---VPEPSGAASCALHSMRAAGDEF 88  
QY 60 -----PG-----GRLAECYVLLRLGITWGVKVSLSYSAAGLAVDCVRQ 98  
DB 89 EERFROAFSEISTQIHVHPGTAAYARFAEVAAGSLFQGVNWKRIVAFVFGAALCAESYVK 148  
QY 99 AQPAMVHALVDLGEFVRKTLATWLRRRGGMTDVL 133  
DB 149 EMSPLPRIODMWYTYLETNLRDWTQNSGWNGL 183

RESULT 8  
BCLX\_CHICK  
ID BCLX\_CHICK STANDARD; PRT; 229 AA.  
AC 007816; 098908;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-X.  
GN BCL2L1 OR BCLX OR BCL-X.  
OS Gallus gallus (Chicken).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC	Gallus.
CC	NCBI_TaxID=9031;
OX	[1]
RN	SEQUENCE FROM N.A. (SHORT FORM).
RP	MEDLINE=93364977; PubMed=8358789;
RX	Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA	Tutka L.A., Mao X., Nunez G., Thompson C.B.;
RA	"bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT	of apoptotic cell death.";
RL	Cell 74:597-608(1993).
RN	[2]
RP	SEQUENCE FROM N.A. (LONG FORM).
RC	STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX	MEDLINE=97264485; PubMed=9110311;
RA	Vilagrasa X., Mezquita C., Mezquita J.;
RT	"differential expression of bcl-2 and bcl-x during chicken
RL	spermatogenesis.";
RL	Mol. Reprod. Dev. 47:26-29(1997).
CC	-1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC	FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC	ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC	ENVELOPE (BY SIMILARITY).
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC	SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC	DEVELOPMENT.
CC	-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC	FUNCTION. IMPACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC	APOPTOTIC ACTIVITY (BY SIMILARITY).
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
CC	EMBL: Z23110; CAAB0657.1; -;
DR	EMBL: U26645; AAB07677.1; -;
DR	PIR: A47537; A47537.
DR	HSSP: P53563; IAF3.
DR	InterPro: IPR002475; BCL2_family.
DR	InterPro: IPR000712; BCL2_BH.
DR	InterPro: IPR003093; BCL2_BH4.
DR	InterPro: IPR004725; BCL2_reg.
DR	Pfam: PF00452; Bcl-2; 1.
DR	Pfam: PF02180; BH4; 1.
DR	SMART: SM00337; BCL; 1.
DR	SMART: SM00265; BH4; 1.
DR	TIGRFAMs: TIGR00865; bcl-2; 1.
DR	PROSITE: PS50062; BCL2_FAMILY; 1.
DR	PROSITE: PS01080; BH1; 1.
DR	PROSITE: PS01258; BH2; 1.
DR	PROSITE: PS01259; BH3; 1.
DR	PROSITE: PS01260; BH4_1; 1.
DR	PROSITE: PS50063; BH4_2; 1.
KW	Apoptosis; Transmembrane; Alternative splicing.
FT	DOMAIN 4 24 BH4.
FT	DOMAIN 82 96 BH3.
FT	DOMAIN 125 144 BH1.
FT	DOMAIN 176 191 BH2.
FT	TRANSMEM 206 223 POTENTIAL.
FT	VARSPPLIC 185 229 ERFVDIAGNMAAEIRKQGEFNNKWLIGTAVAGVLLIGSL
FT	VARSPPLIC 185 229 LSRK -> VRRALP (IN SHORT ISOFORM).
SEQUENCE	229 AA; 25733 MW; A37D3A4D04C0E9D0 CXC64;

Query Match	Similarity	11.8%	Score 104.5	DB 1	Length 229
Best Local Similarity	24.4%	Pred. No. 0.004			
Matches 31	Conservative	23	Mismatches 64	Indels 9	Gaps 2
QY	4	LRRSVPFAAEIMDAEDRMPDTEKELVAQAKKALGREYVHARLLRAGLSWSAPERASAPAGGR	63		
Db	111	111	111	111	111
	66	VHRSLEVEHETIRVSRAD-----VROLRDPADGEFEFLRYRAFSDLTSQLHITGTAVO	117		
QY	64	LAECVTLRLRGITGWKGVSLYSAAAGLAVDCVQAOAPAMHALVDLCGEVRRKTLATW	122		
Db	118	SPEQGVNLEFHDGVNMGRIAVFFSFGALCVESYDKEMKRVILGRIVSWMTYTLTDHLDPW	177		
QY	123	LRRRGW	129		
Db	178	IQENGW	184		
RESULT 9					
BCLX_MOUSE					
ID	BCLX_MOUSE	STANDARD:	PRT:	233	AA.
AC	064373:	060657:	060658:	06138:	
DT	01-NOV-1997	(Rel. 35,	Created)		
DT	01-NOV-1997	(Rel. 35,	Last sequence update)		
DT	15-JUN-2002	(Rel. 41,	Last annotation update)		
DE	Apoptosis regulator Bcl-x.				
GN	BCL2L1 OR BCL2L OR BCLX.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090:				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=2A4B;				
RA	Kanesaki H., Michaud G.Y., Takatsu K., Okuma M.;				
RL	Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).				
RC	STRAIN=C57BL/6; TISSUE=Brain;				
RX	MEDLINE=9531139; PubMed=760790;				
RA	Gonzalez-Garcia M., Perez-Ballesterio R., Ding L., Duan L., Boise L.H.,				
RA	Thompson C.B., Nunez G.;				
RT	"bcl-xL is the major bcl-x mRNA form expressed during murine				
RT	development and its product localizes to mitochondria.";				
RL	Development 120:3033-3042(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TW)).				
RC	TISSUE=Pre-B cell;				
RX	MEDLINE=95052604; PubMed=7963517;				
RA	Fang W., Rivard J.U., Mueller D.L., Behrens T.W.;				
RT	"Cloning and molecular characterization of mouse bcl-x in B and T				
RT	lymphocytes.";				
RL	J. Immunol. 153:4388-4398(1994).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM X(BETA)).				
RC	STRAIN=C57BL/6 X CBA; TISSUE=Thymus;				
RA	MEDLINE=98051053; PubMed=9390687;				
RA	Yang X.-F., Weber G.F., Cantor H.;				
RT	"A novel Bcl-x isoform connected to the T cell receptor regulates				
RT	apoptosis in T cells.";				
RL	Immunity 7:629-639(1997).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97289584; PubMed=9144489;				
RA	Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,				
RA	Ohta S., Seidlin M.F., Nunez G.;				
RT	"Genomic organization, promoter region analysis, and chromosome				
RT	localization of the mouse bcl-x gene.";				
RL	J. Immunol. 158:4750-4757(1997).				
CC	-I- FUNCTION: Potent inhibitor of cell death. Inhibits activation of				
CC	caspases (By similarity). Appears to regulate cell death by				
CC	blocking the voltage-dependent anion channel (VDAC) by binding				
CC	to it and preventing the release of the caspase activator,				



cytochrome c, from the mitochondrial membrane. The Bcl-x(s) isoform promotes apoptosis.

-1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (by similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (by similarity).

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).

-1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S), BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN ACTIVATED.

-1- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN POSTNATAL TISSUES.

-1- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death.

-1- PTM: Proteolytically cleaved by caspases during apoptosis (by similarity). The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (by similarity).

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

-----

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CC -----

DR EMBL: X83574; CAA8557.1; -

DR EMBL: L35049; AAA51039.1; -

DR EMBL: L35048; AAA51040.1; -

DR EMBL: U10102; AAA82174.1; -

DR EMBL: U10101; AAA82173.1; -

DR EMBL: U10100; AAA82172.1; -

DR EMBL: U51279; AAC53460.1; -

DR EMBL: U78031; AAB96881.1; -

DR EMBL: U78030; AAB96881.1; JOINED.

DR HSSP: P53563; IAF3.

DR MGD: MGI:88139; Bcl2L1.

DR InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; Bcl2\_BH.

DR InterPro: IPR003093; Bcl2\_BH4.

DR InterPro: IPR004725; Bcl2-reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRFAMS: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2\_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4\_1; 1.

DR PROSITE: PS50063; BH4\_2; 1.

KV Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.

FT DOMAIN 4 24 BH4.

FT DOMAIN 86 100 BH3.

FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.

FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).

FT VARSPPLIC 109 233 DTFVLDIGNNAEERKGERNNRFLGMYAGVVLGSL

FT FSRK -> VRTPLVCPPLACVSLCEHP (IN ISOFORM BCL-X(BETA)).

FT

FT VARSPPLIC 194 233 LYGNNAAEERKGERNNRFLGTGTAGVVLGSLFSRK

FT -> GHDCGMCAGGLTQSEVTRH (IN ISOFORM BCL-X(DELTA-TM)).

FT

FT SEQUENCE 233 AA: 26132 MW: 2422AC79887E072E CRC64:

SQ

Query Match 11.8%; Score 104; DB 1; Length 233;

Best Local Similarity 26.6%; Pred. No. 0.0045;

Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

QY 66 EVCYLLRIGITWGVKYSLSAAGIACVQAQAPAMHALVDLCGEVVRTLATWLR 125

DB 125 QVNELEFRDGVNWRIVAFSEGCALCVESVDKEMQVLSRIASWATYLNHLPWIOE 184

QY 126 RCGW 129

DB 185 NCGW 188

RESULT 10

BCLX\_RAT

ID BCLX\_RAT STANDARD: PRT: 233 AA

AC P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;

DT 01-OCT-1996 (rel. 34; Created)

DT 01-NOV-1997 (rel. 35; Last sequence update)

DT 15-JUN-2002 (rel. 41; Last annotation update)

DE Apoptosis regulator Bcl-x.

GN BCL2L1 OR BCL2L OR BCLX.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=101116;

[1]

RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).

RA Michaelidis T.M.;

RC TISSUE=Brain;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RA TISSUE=Brain;

RC TISSUE=Brain;

RL Wesselingh S.L., David G.L., Choi S., Veljuna M., Hardwick J.M.;

RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

[3]

RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).

RA TISSUE=Thymus;

RC MEDLINE=96278736; PubMed=8662675;

RX Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;

RA "An additional form of rat Bcl-x, Bcl-xbeta, generated by an

RT unspliced RNA, promotes apoptosis in promyeloid cells.";

RL J. Biol. Chem. 271:13258-13265(1996).

[4]

RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).

RA STRAIN=Sprague-Dawley; TISSUE=ovary;

RC MEDLINE=95129487; PubMed=7828536;

RX Tilly J.L., Tilly K.I., Kenton M.U., Johnson A.L.;

RA "Expression of members of the bcl-2 gene family in the immature rat

RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa

RT cell apoptosis is associated with decreased bax and constitutive

RL bcl-2 and bcl-xlong messenger ribonucleic acid levels.";

RL Endocrinology 136:232-241(1995).

[5]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RX MEDLINE=98010630; PubMed=9346936;

RA Arltomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,

RA Morikawa K.;

RT "Crystal structure of rat Bcl-xL. Implications for the function of

RT the Bcl-2 protein family.";

RL J. Biol. Chem. 272:27886-27892(1997).

CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of

CC caspases (by similarity). Appears to regulate cell death by

CC blocking the voltage-dependent anion channel (VDAC) by binding

CC to it and preventing the release of the caspase activator,

CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and

CC Bcl-x(beta) isoforms promote apoptosis.



DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis; Mitochondrion; Transmembrane.  
 KW Apoptosis; Mitochondrion; Transmembrane.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 8 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;  
 Query Match 11.7%; Score 103; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0057;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 QY 66 EVCYTLRLRLGRTGKGVSVSLXSAAGLAVDCVQAPAMVHALVDCLGFRVKTATWLR 125  
 DB 125 QVLNLEFLFDGVNMGRIVAFFSGALCVESVDKEMQVLSRIATWATYLANDLEPWIOE 184  
 QY 126 RCGM 129  
 DB 185 NCGW 188  
 RESULT 12  
 BCLX\_HUMAN STANDARD: PRT; 233 AA.  
 AC 007817; 092976;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM X(L) AND X(S)).  
 RX MEDLINE=93364977; PubMed=8358789;  
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.,  
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
 RT of apoptotic cell death.";  
 RL Cell 74:597-608(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BETA).  
 RA Inohara N., Ohta S.,  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.  
 RX MEDLINE=95372373; PubMed=7644501;  
 RA Sedlak T.W., Oliva Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,  
 RA Korsmeyer S.J.,  
 RT "Multiple Bcl-2 family members demonstrate selective dimerizations  
 RT with Bax.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).  
 RN [4]  
 RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.  
 RX MEDLINE=96170038; PubMed=8596636;  
 RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,  
 RA Korsmeyer S.J.,  
 RT "Bax-independent inhibition of apoptosis by Bcl-XL.";  
 RL Nature 379:554-556(1996).  
 RN [5]  
 RP STRUCTURE BY NMR OF 1-209.

RX MEDLINE=97172562; PubMed=9020082;  
 RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,  
 RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,  
 RA Thompson C.B., Pesik S.W.,  
 RT "Structure of Bcl-XL-Bak peptide complex: recognition between  
 RT regulators of apoptosis.";  
 RL Science 275:983-986(1997).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.  
 RX MEDLINE=96256675; PubMed=8692274;  
 RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,  
 RA Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,  
 RA Ng S.L., Pesik S.W.,  
 RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed  
 RT cell death.";  
 RL Nature 381:335-341(1996).  
 RN [7]  
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.  
 RX MEDLINE=98118550; PubMed=9435230;  
 RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,  
 RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Veluona M.A.,  
 RA Hardwick J.M.,  
 RT "Modulation of cell death by Bcl-XL through caspase interaction.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-X(S)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC Heterodimerization with BAX does not seem to be required for anti-  
 CC apoptotic activity.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS  
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING  
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING  
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC EMBL; 223116; CAAB0662.1; -;  
 CC EMBL; 223115; CAAB0661.1; -;  
 CC EMBL; U72398; AAB17354.1; -;  
 CC PDB; 1BXL; 29-OCT-97.  
 CC PDB; 1LXL; 21-APR-97.  
 CC PDB; 1MAZ; 21-APR-97.  
 CC Genew; HGNC:992; BCL2L1.  
 CC MIM; 600039; -;  
 CC InterPro; IPR002475; BCL2 family.  
 CC InterPro; IPR000712; Bcl2\_BH.  
 CC InterPro; IPR003093; Bcl2\_BH4.  
 CC InterPro; IPR004725; Bcl2\_reg.

DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KW 3D-structure.  
 FT DOMAIN 4 24 BH4.  
 FT 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 FT SITE 61 61 CLEAVAGE BY CASPASE-1.  
 FT VASAPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 FT VASAPLIC 189 233 DTVELYGNMAAESRKGQERNFMFLGTMVAVAGVILGSL  
 FT FSRK -> VTRKPLVCFPSLASGQSRPTALLLYFLLCWVI  
 FT VGDVDS (IN ISOFORM BCL-X(BETA)).  
 FT D->A: NO CLEAVAGE BY CASPASE-1 NOR BY  
 FT CASPASE-3.  
 FT FRD->VRA: NO HETERODIMERIZATION WITH BAX.  
 FT VNM->AIL: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT GRI->ELN: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT MUTAGEN 138 140 ACTIVITY.  
 FT MUTAGEN 138 138 G->A: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 148 148 G->E: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 156 156 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT MUTAGEN 176 176 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT MUTAGEN 188 189 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY  
 FT BY ABOUT HALF.  
 FT MUTAGEN 189 189 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT CONFLICT 70 70 G->A (IN REF. 1; CAA80661).  
 FT SEQUENCE 233 AA; 26049 MW; E09D3CDD851AE9BE CRC64;  
 Query Match 11.5%; Score 102; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0071;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 QY 66 EVCYVLRGLGTTGWKVSLSYSAAGLAVDCYRQAPAVHALVDCLGFEVKRTLATWRR 125  
 DB 125 QVVELFEDGVNMGRIYAFSEFGALCVESVDKEMQVLSRIAAMATYINDHLEPWIOE 184  
 QY 126 RGGW 129  
 DB 185 NGW 188  
 RESULT 13  
 BAXB\_HUMAN STANDARD; PRT: 218 AA.  
 AC 007814;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, cytoplasmic isoform beta.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RX MEDLINE=93364978; PubMed=8358790;  
 RA Oliva 2.N., Millman C.L., Korsmeyer S.J.;  
 RT "bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
 RT accelerates programmed cell death.";

RL Cell 74:609-619(1993).  
 CC -I- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADONOVIRUS  
 CC HOMOLOG E1B 19K PROTEIN.  
 CC SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.  
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -I- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
 CC ALTERNATIVE SPLICING.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -I- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L22474; AAA03620.1; -  
 DR PIR: B47538; B47538.  
 DR HSSP: Q07817; IMAZ.  
 DR GeneW: HGNC:959; BAX.  
 DR MIM: 600040; -  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR007112; BCL2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR Apoptosis; Alternative splicing.  
 KW Apoptosis; Alternative splicing.  
 FT DOMAIN 59 73 BH3.  
 FT DOMAIN 98 118 BH1.  
 FT DOMAIN 150 165 BH2.  
 FT SEQUENCE 218 AA; 24220 MW; F69DCD70F960192AF CRC64;  
 Query Match 11.3%; Score 100; DB 1; Length 218;  
 Best Local Similarity 22.2%; Pred. No. 0.01;  
 Matches 34; Conservative 25; Mismatches 52; Indels 42; Gaps 5;  
 QY 22 PTDKELVAQAKALGRE-YVHARLLRAGLSWSAPER-SPAP-GGRLAECVTLRLG-- 75  
 DB 13 PTSSQIMKGTGALLQGIQDRAGRMG--GEAPELADLPVPODASTKLSCLKRIGDEL 70  
 QY 76 -----ITWKKVSYLSAAGLAVDCYRQAP 101  
 DB 71 DSNMELQRIAAVDTPDSREVEFFRYAADMFSQGNFMGRVVALFPFASKVLKALCTKVP 130  
 QY 102 AMVHALVDCLEFEVFKRTLATWLRGGTGVLYK 134  
 DB 131 ELIRITMGWTDPLERLRLGHIQDQGGVRLIK 163  
 RESULT 14  
 BCLW\_MOUSE STANDARD; PRT: 193 AA.  
 AC P70345;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-W.  
 GN BCL2L2 OR BCLW.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96358615; PubMed=8761287;  
 RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,  
 RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,  
 RT "bcl-2, a novel member of the bcl-2 family, promotes cell survival.";  
 RL Oncogene 13:665-675(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/10J;  
 RX MEDLINE=98160183; PubMed=9500547;  
 RA Ross A.J., Mayhew K.G., Moss J.E., Parlow A.F., Skinner M.K.,  
 RA Russell L.D., Macgregor G.R.,  
 RT "Testicular degeneration in bclw-deficient mice.";  
 RL Nat. Genet. 18:251-256(1998).  
 CC -1- FUNCTION: PROMOTES CELL SURVIVAL.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND  
 CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,  
 CC AND SALIVARY GLAND.  
 CC -1- DOMAIN: B4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
 CC FUNCTION.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U59746; AAB09056.1; -  
 DR EMBL: AF030769; AAB86430.1; -  
 DR HSP: Q07817; IMAZ.  
 DR MGD: MGI:108052; Bcl2.12.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS00662; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis.  
 KW Apoptosis.  
 FT DOMAIN 9 29 BH4.  
 FT DOMAIN 85 104 BH1.  
 FT DOMAIN 136 151 BH2.  
 SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;  
 Query Match 11.2%; Score 99; DB 1; Length 193;  
 Best Local Similarity 24.3%; Pred. No. 0.011;  
 Matches 27; Conservative 19; Mismatches 63; Indels 2; Gaps 2;  
 OY 22 PTDKELVAQAKALGREYHARLLRAGLSNAPERRASPAPG-GLAEVCTVLLRLGITWCK 80  
 Db 37 PAADPLHQAMRAAGDEF-ETRRFRFTSDLAQLHVTGSAQOQFTQVSDLEFGGPNMGR 95  
 OY 81 VVSLYSAAAGLAVDCYRQAQPAVVAHVLCGLGFEVRRKTLATWLRRCGQWTD 131  
 Db 96 LVAFVFGAALCAESYKNEKPEPLVGOVQDMVAVLLETRLADWTHSSGGMAE 146

RESULT 15  
 ARL\_XENLA  
 ID ARL\_XENLA STANDARD; PRT; 204 AA.  
 AC Q91828;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator R11 (XRL1).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxId=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Head;  
 RX MEDLINE=95331613; PubMed=7607538;  
 RA Cruz-Reyes J., Teta J.R.,  
 RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
 RT cell-survival genes.";  
 RL Gene 158:171-179(1995).  
 CC -1- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
 CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
 CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
 CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X82461; CAA57844.1; -  
 DR HSP: Q07817; IMAZ.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMS: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR Apoptosis; Transmembrane.  
 KW Apoptosis; Transmembrane.  
 FT DOMAIN 101 120 BH1.  
 FT DOMAIN 152 167 BH2.  
 FT TRANSMEM 181 198 POTENTIAL.  
 SQ SEQUENCE 204 AA; 23379 MW; 3BFC6BB6DDA4CA03 CRC64;  
 Query Match 11.1%; Score 98; DB 1; Length 204;  
 Best Local Similarity 26.6%; Pred. No. 0.015;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 OY 66 EVCVTLRLGITGKVVSLYSAAAGLAVDCYRQAQPAVVAHVLCGLGFEVRRKTLATWLR 125  
 Db 97 QVAGELFPGTGNMGRIVAFESFGALCVSANKEMTDLLPRIVQWVNYLEHTLPWMOE 156  
 OY 126 RCGM 129  
 Db 157 NGCM 160

Job time : 6.99217 secs

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## OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 10.6527 Seconds  
(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-8  
Perfect score: 884

Sequence: 1 MEVLRSSVPAAEIMDAFDR.....TICSGRFLKAAPFLUPER 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

1: PIR.73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	15.5	236	2	gene bcl-2 protein
2	133	15.0	239	1	transforming prote
3	131.5	14.9	236	2	BCL-2 - rat (fragm
4	131	14.8	236	1	B-cell lymphoma 2
5	130	14.7	236	1	transforming prote
6	124	14.0	205	1	transforming prote
7	123	13.9	199	1	transforming prote
8	116.5	13.2	216	2	transforming prote
9	115.5	13.1	233	2	transforming prote
10	114	12.9	227	2	apoptosis regulato
11	107	12.1	232	2	transforming prote
12	104.5	11.8	190	2	apoptosis regulato
13	104	11.8	214	2	bcl-2-associated p
14	104	11.8	233	2	bcl-x long - mouse
15	104	11.8	233	2	BCL-X protein - ra
16	102	11.5	233	2	apoptosis regulato
17	100	11.3	218	2	BCL-2-associated p
18	97.5	11.0	233	2	BCL-X-long - rat
19	97	11.0	179	2	Bax-delta protein
20	95	10.7	192	2	bcl-2-associated p
21	95	10.7	211	2	Bak protein - huma
22	93	10.5	133	2	bcl-2-associated p
23	92.5	10.5	143	2	bcl-2-associated p
24	92	10.4	192	2	hemopoietic-specif
25	85.5	9.7	172	2	cdm-2 protein - hu
26	85	9.6	211	2	e antigen precurs
27	84	9.5	212	2	carbamoyl-phosphat
28	83	9.4	1115	2	probable polyketid
29	82	9.3	2126	2	

30	80.5	9.1	2326	2	T29140	hypothetical prote
31	79.5	9.0	822	2	AE2404	DNA helicase limpo
32	79.5	9.0	860	2	C82750	mannosyltransferas
33	78.5	8.9	319	2	T10583	hypothetical prote
34	78.5	8.9	540	2	T34702	hypothetical prote
35	78	8.8	183	2	S53181	core antigen - hep
36	78	8.8	212	2	S25651	e antigen precurs
37	78	8.8	356	2	G81907	probable integral
38	78	8.8	419	2	A83133	probable MFS trans
39	77.5	8.8	154	2	I81894	gene bcl-2 protein
40	77.5	8.8	364	2	AH1857	anthranilate phosph
41	77.5	8.8	412	2	T37042	probable nitrate/n
42	77.5	8.8	2291	1	A46147	spectrin beta chain
43	77	8.7	175	2	I39055	Bcl-2 related - hu
44	77	8.7	214	2	S47409	e antigen precurs
45	76.5	8.7	482	2	C86442	probable amino aci

## ALIGNMENTS

## RESULT 1

153744 gene bcl-2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999

C:Accession: I53744

R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.

Gene 140, 291-292, 1994

A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.

A:Reference number: I53744; MUID:94193015; PMID:8144041

A:Accession: I53744

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236 <RES>

A:Cross-references: GB:L14680; NID:q408946; PIDN:AAA53662.1; PID:q408947

C:Genetics:

A:Gene: bcl-2

C:Superfamily: bcl transforming protein

Query Match	Best Local Similarity	Matches	45;	Conservative	25;	Mismatches	57;	Indels	92;	Gaps	5;
OY	28	VQAQALG-----REYVHARLRLAGLSW-----SAPERASPAAG-----	11	11	11	11	11	11	11	11	11
DB	1	MAQAGRTGYDNEIYMKYIHYKLSQRYEMDTGDEDSAPLRAPPGILFSPQESNRTPA	60								
OY	62	-----	61								
DB	61	VHRDFAARTSPRLPVANAGPALSPVPVHLTLRRAGDDFSRRYRDEPAEMSQLHLTP	120								
OY	62	-----GRLAECVTLRLGLTGKQVSLTSAAGLAVDCYRQAPMVAHNLVDCLOCFPRK	117								
DB	121	FTARGRFAIVDELFRRDQVGMGRIVAFEEFGVCMGVSNRMSPLVNIALMTEYLNR	180								
OY	118	TLATWLRRRGWTDVLKCY-VSTKPGPFRSHML-VATLLCS	154								
DB	101	HHHTWIDNGMDAFVELYGPMSRPLDFPSWLSLTKLLS	219								

## RESULT 2

153744 transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999

C:Accession: G37332; A29409; S02452; A24428; A27622; B27622

R:Enguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va

A:Reference number: A37332; MUID:9237524; PMID:1508712

A:Accession: G37332

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

[illegible]

```

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: 167432
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A:Reference number: 153295; MUID:95129487; PMID:7828536
A:Accession: 167432
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004379
C:Superfamily: bcl transforming protein

Query Match 14.9%; Score 131.5; DB 2; Length 236;
Best Local Similarity 18.9%; Pred. No. 1.6e-05;
Matches 44; Conservative 27; Mismatches 61; Indels 101; Gaps 5;

QY 28 VAQAALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61
||| | | | | | | | | | | | | | | | |
Db 1 MAQAQRTGYDNRREIYMKYIHKLSQRYEWDGSDAPLRRAPIPGISFQPSNPTPA 60
----- 61

QY 62 ----- 61
VHRDJAARTSPLRLPVANAGPALSPVPVYHLLTRRAGDGSRRYRRDFAEMSQLHLTP 120

QY 62 ----GRLAECVTLLRLGITWGVSLYSAAGLAVDCVROAQPAMVHALVDCGEEYRK 117
|| | | | | | | | | | | | | | | | | |
Db 121 FTARGRFATVVEELFRDGVNMGRIYAFEEFGVCMVESVNBEMVPLVNIALMPTYELNR 180

QY 118 TLATWLRRRGGCTDYLKCV-VSTKPGFRSHW-----LYATLGSFGAFL 159
| | | | | | | | | | | | | | | | | |
Db 181 HLHTWIDQNGWDFAVELYGPMPRLFPDSWSQSLKTLTSLALVGCITLGAFL 233

RESULT 4
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7383
R:Biometric, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A:Reference number: JC7383
A:Contents: Ovary
A:Accession: JC7383
A:Molecule type: mRNA
A:Residues: 1-236 <TOM>
A:Cross-references: GB:AJ271720
C:Comment: This protein has anti-apoptotic function, and supports cell survival.
C:Genetics:
A:Gene: bcl-2
C:Superfamily: bcl transforming protein
C:Keywords: B-cell lymphoma; ovary

Query Match 14.8%; Score 131; DB 2; Length 236;
Best Local Similarity 19.6%; Pred. No. 1.8e-05;
Matches 43; Conservative 27; Mismatches 57; Indels 92; Gaps 5;

QY 28 VAQAALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61
||| | | | | | | | | | | | | | | | |
Db 1 MAQAQRTGYDNRREIYMKYIHKLSQRYEWDGSDAPLRRAPIPGISFQPSNPTPA 60
----- 61

QY 62 ----- 61
VHRDMAATSPRLPIVATGTPSLSPVPVYHLLTRRADDSSRRYRRDFAEMSQLHLTP 120

QY 62 ----GRLAECVTLLRLGITWGVSLYSAAGLAVDCVROAQPAMVHALVDCGEEYRK 117
|| | | | | | | | | | | | | | | | | |
Db 121 FTARGRFATVVEELFRDGVNMGRIYAFEEFGVCMVESVNBEMVPLVNIALMPTYELNR 180

QY 118 TLATWLRRRGGCTDYLKCV-VSTKPGFRSHW-VATLGS 154

```



Db 181 HLHTWIDNGMDAFVELXGSPVRLPFDPSWLSKTLTLLS 219

RESULT 5

TRANSAL

transforming protein bcl-2-alpha - mouse

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: A25960; E37332

R:Neglini, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: A25960

A:Molecule type: DNA

A:Residues: 1-236 <NEG>

A:Cross-references: GB:LJ1533; GB:M16506; NID:9468336; PIDN:AAA37282.1; PID:9387109

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: E37332

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: DNA

A:Residues: 1-33,'E',34-220,'AL',223-236 <EGU>

C:Genetics:

A:Gene: BCL2

A:Introns: 192/3

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 14.7% Score 130; DB 1; Length 236;  
Best Local Similarity 19.6% Pred. No. 2,2e-05;

Matches 43; Conservative 27; Mismatches 57; Indels 92; Gaps 5;

QY 28 VAQAKALG-----REYVHARLLRAGLSW-----SAPERASPARG----- 61

Db 1 MAQAGRTGYDNRITWKYIHYKLSQRYEMDAGDADAPLGAAPPTGIFSFOPESNMPMA 60

QY 62 ----- 61

Db 61 VIREMAARTSPRLPLVATGAPALSPVPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120

QY 62 ----GRLAECYVLLRLGITGKQVSLYSAAAGLAVDCYRQAPAMVHALVDCLEGFVRK 117

Db 121 FTARGGFATVVEELFRDGVNMGRIYAFPEFGVGVCEVSNREMSPLVDNALMTEYLNR 180

QY 118 TLATWLRGGRGWTDLKCV-VSTKPGCFRSHWL-VATLCS 154

Db 181 HLHTWIDNGMDAFVELXGSPVRLPFDPSWLSKTLTLLS 219

RESULT 6

TRANSAL

transforming protein bcl-2, splice form beta - human

N:Alternate names: apoptosis regulator bcl-2

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 15-Oct-1999

C:Accession: B29409; I52566; D37332

R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene

A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: B29409

A:Molecule type: mRNA

A:Residues: 1-205 <TSU>

A:Cross-references: GB:M13995; NID:9179368; PIDN:AAA51814.1; PID:9179369

R:Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.

Blood 79, 229-237, 1992

A:Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-H

A:Reference number: I52566; MUID:92096610; PMID:1339299

A:Accession: I52566

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-131 <TAN>

A:Cross-references: GB:S72602; NID:9241046; PIDN:AAD14111.1; PID:94261811

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: D37332

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 1-33,'E',34-95,'T',97-109,'R',111-205 <EGU>

C:Genetics:

A:Gene: GDB:BCL2

A:Cross-references: GDB:119031; OMIM:151430

A:Map position: 18q21.3-18q21.3

C:Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr

Query Match 14.0% Score 124; DB 1; Length 205;  
Best Local Similarity 17.9% Pred. No. 7,6e-05;

Matches 32; Conservative 22; Mismatches 39; Indels 86; Gaps 2;

QY 37 EYVHARLLRAGLSW-----SAPERASPARG----- 61

Db 17 KYIHYKLSQRYEMDAGDADAPLGAAPPTGIFSFOPESNMPMA 76

QY 62 ----- 61

Db 77 APCGAAGPALSPVPCVHLTLRRAGDDFSRRYRGDFAEMSSQLHLTPFTARGFATVVEE 136

QY 71 LRLGITGKQVSLYSAAAGLAVDCYRQAPAMVHALVDCLEGFVRK 129

Db 137 LFRDGVNMGRIYAFPEFGVGVCEVSNREMSPLVDNALMTEYLNRHLHTWIDNGW 195

RESULT 7

TRANSAL

transforming protein bcl-2-beta - mouse

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: B25960

R:Neglini, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: B25960

A:Molecule type: DNA

A:Residues: 1-199 <NEG>

A:Cross-references: GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:9387110

C:Genetics:

A:Gene: BCL2

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; transforming protein

Query Match 13.9% Score 123; DB 1; Length 199;  
Best Local Similarity 19.0% Pred. No. 9,2e-05;

Matches 38; Conservative 24; Mismatches 46; Indels 92; Gaps 4;

QY 28 VAQAKALG-----REYVHARLLRAGLSW-----SAPERASPARG----- 61

Db 1 MAQAGRTGYDNRITWKYIHYKLSQRYEMDAGDADAPLGAAPPTGIFSFOPESNMPMA 60

QY 62 ----- 61

Db 61 VIREMAARTSPRLPLVATGAPALSPVPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120

QY 62 ----GRLAECYVLLRLGITGKQVSLYSAAAGLAVDCYRQAPAMVHALVDCLEGFVRK 117

Db 121 FTARGGFATVVEELFRDGVNMGRIYAFPEFGVGVCEVSNREMSPLVDNALMTEYLNR 180

OY 118 TLATWLRRCGWTDLKCV 137  
 |||: |||: |||:  
 Db 181 HLHTWIDONGW -VGACLV 198

## RESULT 8

B37332  
 transforming protein (bcl-2-beta) - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 24-Apr-1998  
 C:Accession: B37332; S35452  
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
 A:Reference number: A37332; MUID:92375724; PMID:1508712  
 A:Accession: B37332  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-216 <EGU>  
 A:Cross-references: EMBL:D11381; EMBL:D11382  
 C:Superfamily: bcl transforming protein

Query Match 13.2%; Score 116.5; DB 2; Length 216;  
 Best Local Similarity 16.6%; Pred. No. 0.00044;  
 Matches 32; Conservative 22; Mismatches 54; Indels 85; Gaps 2;

OY 37 EYVHARLLRAGLSAPRASPAP----- 60  
 |||: |||: |||: |||:  
 Db 17 KYIHKLSQRCGYDMAAGEDRPVPAPAPAAVAAGASSHHRRPPGSAASEVPP 76  
 OY 61 -----GRLAEVCTVLLRLGI 76  
 |||: |||: |||: |||:  
 Db 77 AEGLRPAPGVHLLRQAGDEFSSRRYQDFQMSGOLHLPPTTAGRFVAVVEELFRDGV 136  
 OY 77 TWGKVVSLYSAAAGLAVDCVROAPAMVHALVDCGEFVRKTLATLRRGGMTDLKCV 136  
 |||: |||: |||: |||: |||: |||: |||:  
 Db 137 NMGRIVAFEEFGVWCVSVNREMSPLVDNLTMTETLNRHLHWIDONGWVAAACSL 196  
 OY 137 VSTRKPFERSHMLV 149  
 |||: |||: |||:  
 Db 197 SST-----GGMWLV 204

## RESULT 9

A37332  
 transforming protein (bcl-2-alpha) - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 23-Feb-1997  
 C:Accession: A37332; S35453  
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
 A:Reference number: A37332; MUID:92375724; PMID:1508712  
 A:Accession: A37332  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-233 <EGU>  
 A:Cross-references: EMBL:D11381  
 C:Genetics:  
 A:Introns: 189/3  
 C:Superfamily: bcl transforming protein  
 C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 13.1%; Score 115.5; DB 2; Length 233;  
 Best Local Similarity 16.4%; Pred. No. 0.0006;  
 Matches 35; Conservative 26; Mismatches 62; Indels 91; Gaps 3;

OY 37 EYVHARLLRAGLSAPRASPAP----- 60  
 |||: |||: |||: |||:  
 Db 17 KYIHKLSQRCGYDMAAGEDRPVPAPAPAAVAAGASSHHRRPPGSAASEVPP 76  
 OY 61 -----GRLAEVCTVLLRLGI 76  
 |||: |||: |||: |||:

Db 77 AEGLRPAPGVHLLRQAGDEFSSRRYQDFQMSGOLHLPPTTAGRFVAVVEELFRDGV 136  
 OY 77 TWGKVVSLYSAAAGLAVDCVROAPAMVHALVDCGEFVRKTLATLRRGGMTDLKCV 136  
 |||: |||: |||: |||: |||: |||: |||:  
 Db 137 NMGRIVAFEEFGVWCVSVNREMSPLVDNLTMTETLNRHLHWIDONGWVAAFAVELY 196  
 OY 137 -VSTRKPFERSHMLV-----LVATLCSFGRFL 159  
 |||: |||: |||: |||:  
 Db 197 GNSMRPLDFEWSISLKITLILVLVGCITLGVYL 230

## RESULT 10

JE0203  
 apoptosis regulator bcl-x isoform - human  
 N:Alternate names: h-bcl-xbeta  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 16-Jul-1999  
 C:Accession: JE0203  
 R:Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.  
 Biochem. Biophys. Res. Commun. 248, 147-152, 1998  
 A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.  
 A:Reference number: JE0203; MUID:98340865; PMID:9675101  
 A:Accession: JE0203  
 A:Molecule type: mRNA  
 A:Residues: 1-227 <BAN>  
 A:Cross-references: GB:U72398; NID:91622940; PIDN:AAB17354.1; PID:91622941  
 C:Genetics:  
 A:Gene: bcl-x  
 A:Map position: 20  
 C:Superfamily: bcl transforming protein

Query Match 12.9%; Score 114; DB 2; Length 227;  
 Best Local Similarity 29.3%; Pred. No. 0.00083;  
 Matches 24; Conservative 15; Mismatches 41; Indels 2; Gaps 1;

OY 66 EYCVTLRLGITWCKVSLYSAAAGLAVDCVROAPAMVHALVDCGEFVRKTLATLRR 125  
 |||: |||: |||: |||: |||: |||: |||:  
 Db 125 QVNELEFRDGVNMGRIVAFEEFGALCVESYDKEMQVLVSRILAMMATYLLNDHLEPWIOE 184  
 OY 126 RGGW--TDVLRKCVVSTRKPFERS 145  
 |||: |||: |||: |||:  
 Db 185 NGGWRTKPLVCPFSLASGORS 206

## RESULT 11

S24390  
 transforming protein (Bcl-2) homolog - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
 C:Accession: S24390  
 R:Caals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.  
 Biochim. Biophys. Acta 1132, 109-113, 1992  
 A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homolog  
 A:Reference number: S24390; MUID:92375084; PMID:1511008  
 A:Accession: S24390  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-232 <CAZ>  
 A:Cross-references: EMBL:Z11961; NID:962969; PIDN:CAA78018.1; PID:962970  
 C:Superfamily: bcl transforming protein  
 C:Keywords: mitochondrion; transmembrane protein

Query Match 12.1%; Score 107; DB 2; Length 232;  
 Best Local Similarity 16.0%; Pred. No. 0.0042;  
 Matches 34; Conservative 26; Mismatches 63; Indels 90; Gaps 3;

OY 37 EYVHARLLRAGLSAPRASPAP----- 60  
 |||: |||: |||: |||:  
 Db 17 KYIHKLSQRCGYDMAAGEDRPVPAPAPAAVAAGASSHHRRSPARLLVRCPR 76  
 OY 61 -----GRLAEVCTVLLRLGIT 77  
 |||: |||: |||: |||:  
 Db 77 LRCAAPPGVHLLRQAGDEFSSRRYQDFQMSGOLHLPPTTAGRFVAVVEELFRDGV 136



Db 125 QVWNELEFRDGVNMGRIVAFSEGCALCVESVDKENOVLSRIASWMATYLNDDHLEFWIOE 184  
Oy 126 RSGW 129  
Db 185 NGW 188

Search completed: April 29, 2003, 11:26:37  
Job time : 11.6527 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:16:46 ; Search time 25.9661 Seconds  
(without alignments)  
872.393 Million cell updates/sec

Title: US-09-682-667-8  
Perfect score: 884  
Sequence: 1 MEVLRRSSVFPAEIMDAFDR.....TLCSPGRFLKAFLLPER 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database :  
A.Geneseq\_101002.\*  
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
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19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	884	100.0	170	20	AAV14156 Human Bcl protein se
2	853	96.5	170	20	AAV14154 Human Bcl protein se
3	852.5	96.4	213	20	AAV14155 Human Bcl protein se
4	828.5	93.7	213	20	AAV14153 Human Bcl protein se
5	820.5	92.8	213	21	AAAB41444 Human ORFX ORF1208
6	484	54.8	134	22	AAAB85665 Human Bcl-2-like p
7	484	54.8	176	21	AAAB58949 Breast and ovarian
8	169.5	19.2	247	22	ABBB63760 Drosophila melanog
9	169	19.1	846	22	ABBB64401 Drosophila melanog
10	135	15.3	272	19	AAV21120 Human bcl2 proto-o

11	134	15.2	239	17	AAW02383 Human BCL2. Homo
12	134	15.2	239	22	AAG64036 Human Bcl-2 protei
13	134	15.2	239	22	AAG64038 Human Bcl-2 protei
14	133	15.0	239	9	AAE80987 Sequence of bcl-2-
15	133	15.0	239	14	AAE42312 Bcl-2 oncogene pro
16	133	15.0	239	16	AAE70331 Human bcl-2 protei
17	133	15.0	239	19	AAE71404 Human bcl-2. Homo
18	133	15.0	239	19	AAE40217 Human bcl-2. Homo
19	133	15.0	239	20	AAE87810 A human Bcl-2 prot
20	133	15.0	239	20	AAE87812 Human Bcl-2 alph
21	133	15.0	239	22	AAE08573 Human Bcl-2 protei
22	133	15.0	239	22	AAE64035 Human Bcl-2 protei
23	133	15.0	239	22	AAE64037 Human Bcl-2 protei
24	133	15.0	239	22	AAE74127 Human bcl-2. Homo
25	133	15.0	239	22	AAE74129 Human bcl-2alpha.
26	133	15.0	239	22	AAE48288 Human BCL-2 protei
27	133	15.0	239	22	AAE35130 Human Bcl-2. Homo
28	133	15.0	239	22	AAE50537 Human Bcl-2 protei
29	133	15.0	239	23	AAE75986 Protein sequence..
30	133	15.0	239	23	AAU76553 Human Bcl-2 poly
31	133	15.0	239	23	ABE05227 Human D34A caspase
32	131	14.8	239	22	AAE64039 Human Bcl-2 protei
33	130	14.7	229	17	AAE01021 Apoptosis-blo
34	130	14.7	229	20	AAE94348 Human Bcl-2 mutant
35	130	14.7	229	20	AAE87811 A murine Bcl-2 pro
36	130	14.7	236	22	AAE74128 Murine bcl-2. Mus
37	130	14.7	236	22	AAE35131 Murine Bcl-2. Mus
38	130	14.7	236	23	AAU76554 Murine Bcl-2 poly
39	130	14.7	239	15	AAE47344 Human oncogene bcl
40	128.5	14.5	232	17	AAE01020 Apoptosis-blo
41	128.5	14.5	232	20	AAE94347 Human Bcl-2 mutant
42	125.5	14.2	239	21	AAE69203 Amino acid sequenc
43	125	14.1	239	17	AAE01018 Apoptosis-blo
44	125	14.1	239	20	AAE94345 Human Bcl-2 wild-t
45	124	14.0	205	16	AAE70332 Human bcl-2 protei

## ALIGNMENTS

RESULT 1  
AAV14156  
ID AAV14156 standard; Protein; 170 AA.  
XX  
AC AAV14156;  
XX  
DT 27-JUL-1999 (first entry)  
XX  
DE Human Bcl protein sequence.  
XX  
XX Bcl protein; Bcl-2-related ovarian killer; BHL1 variant; endometriosis;  
KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
XX  
XX proliferative disorder; human.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO924453-A1.  
XX  
PD 20-MAY-1999.  
XX  
PF 04-NOV-1998; 98WO-US23523.  
XX  
PR 07-NOV-1997; 97US-0064943.  
XX  
(STRD ) UNIV IELAND STANFORD JUNIOR.  
XX  
PI Hsu SY, Hsueh AW.  
XX  
DR WPI: 1999-327356/27.  
XX N-PSDB; AAX61106.  
XX

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
protein and its related gene  
PS Claim 2; Page 57-58; 62pp; English.  
XX  
XX  
CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.  
XX  
XX Sequence 170 AA:  
SQ  
Query Match 100.0%; Score 884; DB 20; Length 170;  
Best Local Similarity 100.0%; Pred. No. 4.9e-93;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MEVLRSSVFFAEIMDADRDPTDKELYAQAALGREYVHARLHAGLSMSAPERASPAP 60  
DB 1 MEVLRSSVFFAEIMDADRDPTDKELYAQAALGREYVHARLHAGLSMSAPERASPAP 60  
OY 61 GGRLAECVTLRLGITGKVVSLYSAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
DB 61 GGRLAECVTLRLGITGKVVSLYSAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
OY 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCSFGRFKAAFFLLPER 170  
DB 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCSFGRFKAAFFLLPER 170  
RESULT 2  
AAV14154  
ID AAV14154 standard; Protein: 170 AA.  
XX  
XX AAV14154;  
XX  
XX 27-JUL-1999 (first entry)  
XX  
XX Rat Bok protein sequence.  
XX  
XX Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
XX pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
XX reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
XX ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
XX proliferative disorder; rat.  
XX  
XX Rattus rattus.  
XX  
XX WO9924453-A1.  
XX  
XX 20-MAY-1999.  
XX  
XX PD 04-NOV-1998; 98WO-US23523.  
XX  
XX PF 07-NOV-1997; 97US-0064943.  
XX  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
XX Hsu SY, Hsueh AJW;  
XX

DR WPI; 1999-327356/27.  
DR N-PSDB; AAX61104.  
XX  
XX  
PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
protein and its related gene  
PS Claim 2; Page 54-55; 62pp; English.  
XX  
XX  
CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.  
XX  
XX Sequence 170 AA:  
SQ  
Query Match 96.5%; Score 853; DB 20; Length 170;  
Best Local Similarity 97.6%; Pred. No. 1.7e-89;  
Matches 166; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 MEVLRSSVFFAEIMDADRDPTDKELYAQAALGREYVHARLHAGLSMSAPERASPAP 60  
DB 1 MEVLRSSVFFAEIMDADRDPTDKELYAQAALGREYVHARLHAGLSMSAPERASPAP 60  
OY 61 GGRLAECVTLRLGITGKVVSLYSAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
DB 61 GGRLAECVTLRLGITGKVVSLYSAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
OY 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCSFGRFKAAFFLLPER 170  
DB 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCSFGRFKAAFFLLPER 170  
RESULT 3  
AAV14155  
ID AAV14155 standard; Protein: 213 AA.  
XX  
XX AAV14155;  
XX  
XX 27-JUL-1999 (first entry)  
XX  
XX Human Bok protein sequence.  
XX  
XX Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
XX pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
XX reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
XX ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
XX proliferative disorder; human.  
XX  
XX Homo sapiens.  
XX  
XX WO9924453-A1.  
XX  
XX PN 20-MAY-1999.  
XX  
XX PD 04-NOV-1998; 98WO-US23523.  
XX  
XX PF 07-NOV-1997; 97US-0064943.  
XX  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
XX

XX Hsu SY, Hsueh AJW;  
 PI  
 XX WPI: 1999-327356/27.  
 DR N-PSDB; AAX61105.  
 XX  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 XX  
 PS Claim 2; Page 55-56; 62pp; English.  
 XX  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 XX  
 SQ Sequence 213 AA;  
 Query Match 96.4%; Score 852.5; DB 20; Length 213;  
 Best Local Similarity 79.8%; Pred. No. 2,66-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;  
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 DB 1 MEVLRSSVFAEIMDAFDRMPTDEKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 QY 61 GGRLAEVCTVLLRL-----GTT 77  
 DB 61 GGRLAEVCTVLLRLGDELEQIRPSYRVNVARQLHPLQSEPVVTDATFLAVAGHIFSAGIT 120  
 QY 78 WGVVSLYSAAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 137  
 DB 121 WGVVSLYSAAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 180  
 QY 138 STKPGFRSHMLVATLCSFGRLKAFLLP 170  
 DB 181 STKPGFRSHMLVATLCSFGRLKAFLLP 213  
 RESULT 4  
 AAY14153  
 ID AAY14153 standard; Protein: 213 AA.  
 AC AAY14153;  
 XX  
 XX 27-JUL-1999 (first entry)  
 DE Rat Bok protein sequence.  
 XX  
 KW Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; rat.  
 XX  
 OS Rattus rattus.  
 XX  
 XX W09924453-A1.  
 XX

PD 20-MAY-1999;  
 XX  
 XX 04-NOV-1998; 98WO-US23523.  
 XX  
 XX 07-NOV-1997; 97US-0064943.  
 XX  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Hsu SY, Hsueh AJW;  
 XX  
 DR WPI: 1999-327356/27.  
 DR N-PSDB; AAX61103.  
 XX  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 XX  
 PS Claim 2; Page 53-54; 62pp; English.  
 XX  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 XX  
 SQ Sequence 213 AA;  
 Query Match 93.7%; Score 828.5; DB 20; Length 213;  
 Best Local Similarity 78.4%; Pred. No. 1,5e-86;  
 Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;  
 QY 1 MEVLRSSVFAEIMDAFDRMPTDEKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRSSVFAEIMDAFDRMPTDEKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 QY 61 GGRLAEVCTVLLRL-----GTT 77  
 DB 61 GGRLAEVCTVLLRLGDELEQIRPSYRVNVARQLHPLQSEPVVTDATFLAVAGHIFSAGIT 120  
 QY 78 WGVVSLYSAAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 137  
 DB 121 WGVVSLYSAAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 180  
 QY 138 STKPGFRSHMLVATLCSFGRLKAFLLP 170  
 DB 181 STKPGFRSHMLVATLCSFGRLKAFLLP 213  
 RESULT 5  
 AAB41444  
 ID AAB41444 standard; Protein: 213 AA.  
 AC AAB41444;  
 XX  
 XX 08-FEB-2001 (first entry)  
 DE Human ORF1208 polypeptide sequence SEQ ID NO:2416.  
 XX  
 KW Human; open reading frame; ORF; detection; cytosolic; hepatotropic;  
 KW vulnary; antiproliferative; antiparkinsonian; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;





Db 11 AROLHISL-----QSEPVVTDALFVAGHIFSAITGKVVSLYAVAGLAVDCVROAQ 64  
 QY 101 PAMVHALVDCGEEFYRKLTATWLRRRGGMTDVLKCVSTKPGFBSHMLVATLCSFGRELK 160  
 Db 65 PAMVHALVDCGEEFYRKLTATWLRRRGGMTDVLKCVSTDPGLRSHMLVVALCSFGRELK 124  
 QY 161 AAFVLLPER 170  
 Db 125 AAFVLLPER 134

RESULT 7  
 AAB58949  
 ID AAB58949 standard; Protein: 176 AA.  
 AC AAB58949;  
 DT 27-MAR-2001 (first entry)  
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.  
 KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KW neurotropic; neuriprotective; antiviral; anti-allergic; hepatotropic;  
 KW antibacterial; anti-inflammatory; antitumor; antiviral; anticonvulsant;  
 KW Addison's disease; allergic; autoimmune haemolytic anaemia;  
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KW cardiovascular disorder; wound healing; neurological disease.  
 OS Homo sapiens.  
 XX WO20005173-A1.  
 XX 21-SEP-2000.  
 XX 08-MAR-2000; 2000WO-US05881.  
 XX 12-MAR-1999; 99US-0124270.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM;  
 XX WPI: 2000-611515/58.  
 XX N-PSDB: AAF21852.  
 XX Claim 11; Page 1103; 1299pp; English.

Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; neurotropic; neuriprotective; antiviral; anti-allergic; hepatotropic; antibacterial; anti-inflammatory; antitumor; antiviral; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and antagonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as

CC cerebral anoxia and epilepsy; and infectious diseases.  
 XX Sequence 176 AA;  
 SQ Query Match 54.8%; Score 484; DB 21; Length 176;  
 Best Local Similarity 73.8%; Pred. No. 3.2e-47;  
 Matches 96; Conservative 5; Mismatches 23; Indels 6; Gaps 1;

QY 41 ARLRAGISWSAPERASAPGRLAEVCTVLRIGITGKVVSLYSAAGLAVDCVROAQ 100  
 Db 53 AROLHISL-----QSEPVVTDALFVAGHIFSAITGKVVSLYAVAGLAVDCVROAQ 106  
 QY 101 PAMVHALVDCGEEFYRKLTATWLRRRGGMTDVLKCVSTKPGFBSHMLVATLCSFGRELK 160  
 Db 107 PAMVHALVDCGEEFYRKLTATWLRRRGGMTDVLKCVSTDPGLRSHMLVVALCSFGRELK 166  
 QY 161 AAFVLLPER 170  
 Db 167 AAFVLLPER 176

RESULT 8  
 ABB63760  
 ID ABB63760 standard; Protein: 247 AA.  
 AC ABB63760;  
 DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster polypeptide SEQ ID NO 18072.  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 KW Drosophila melanogaster.  
 OS WO200171042-A2.  
 XX 27-SEP-2001.  
 XX 23-MAR-2001; 2001WO-US09231.  
 XX 23-MAR-2000; 2000US-191637P.  
 XX 11-JUL-2000; 2000US-0614150.  
 XX (PEKE ) PE CORP NY.  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI: 2001-656860/75.  
 XX N-PSDB: ABL07863.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -  
 XX Disclosure: SEQ ID NO 18072; 21pp + sequence listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AAB57737-ABB72072).  
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 247 AA;  
 SQ Query Match 19.2%; Score 169.5; DB 22; Length 247;

[illegible]

XX	RESULT 9
AC	ABB64401
ID	ABB64401 standard; Protein: 846 AA.
XX	
AC	ABB64401;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster polypeptide SEQ ID NO 19995.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide;
RN	pharmaceutical.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US09231.
XX	
PR	23-MAR-2000; 2000US-191637P.
PA	11-JUL-2000; 2000US-0614150.
XX	
PE	(PEKE ) PE CORP NY.
XX	
PI	Venter JC, Adams M, Li PWD, Myers EW;
XX	
DR	WPI: 2001-656860/75.
DR	N-PSTD: ABL08504.
XX	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signalling and cell-cell
PT	interactions -
XX	
PS	Disclosure; SEQ ID NO 19995; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	useful in developmental biology and in elucidating cell signalling and
CC	cell-cell interactions in higher eukaryotes for the development of
CC	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC	sequences (ABL01840-ABL16175) and the encoded proteins
CC	(ABB57737-ABB72072).
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
XQ	Sequence 846 AA;

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Query Match      19.1%  Score 169:  DB 22:  Length 846;
Best Local Similarity 27.6%  Pred. No. 2.9e+10;
Matches 43;  Conservative 17;  Mismatches 44;  Indels 52;  Gaps 3;

26 ELVAQAKALGVEYHARLRAG-LSMSAPR----- 55
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Db	96	DIINGKCLGGYINARLRAGVLNRKVTQRRNLIDPGSSHYVEYEPALNSGEELER	155
QY	56	-----ASAPRGRLAE-----VTVLLRLGITGKGVSLYSAAGLAV	93
Db	156	MHPRYVTNISKRLSPAPGSELEDSMAPMLNLVAKDLFRSSITWGKLIISFVCGGFPI	215
QY	94	DCVROQAPAMVHALVDCLGEEFYRKTLLATWLRRRGW	129
Db	216	DCVROGHFDYLOCLTIDGLAEIIEEDLVYVLLIDNGW	251

RESULT 10  
 AA121120  
 ID AA121120 standard; Protein; 272 AA.

XX	Human bcl2 proto-oncogene wild type protein fragment 17.
DE	
XX	
XX	
AC	AAV21120;
XX	
DT	22-JUL-1999 (first entry)
XX	
XX	
XX	Homo sapiens.
OS	
XX	MO98645322-A2.
PN	
XX	15-OCT-1998.
PD	
PE	02-APR-1998; 98WO-IB00705.
XX	
ER	10-APR-1997; 97US-0043163.
XX	
PA	(UYUT-) RIJKSUNIV UTRECHT.
PA	(ROYA-) ROYAL NETHERLANDS ACADEMY OF SCIENCES.
PA	(UYRO-) UNIV ROTTERDAM ERASMUS.
PL	Burbach JPH, Grosveld FG, Van Leeuwen FW;
DR	WPI: 1998-609901/51.
XX	N-PSDB: AAV75766.
PT	Diagnosing disease by detecting frameshift mutations in RNA or
PT	neurological diseases, particularly Alzheimer's disease, and also
PT	for treatment and prevention with specific ribozymes or wild-type
RNA	
XX	
XX	Disclosure: Figure 15: 258bp; English.
XX	
CC	This invention describes a novel method for the diagnosis of a disease
CC	caused by, or associated with, an RNA molecule that has a frameshift
CC	mutation. The method is used to diagnose age-related diseases, especially
CC	cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC	disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II
CC	multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC	and many others listed) or susceptibility to these disorders. The method
CC	allows a definitive diagnosis of Alzheimer's disease in living patients,
CC	at an early stage. It is based on the observation that disease may be
CC	caused by mutations in RNA rather than DNA. The invention describes the
CC	use of neuronal system RNA molecules, specifically proteins including
CC	beta-amyloid precursor protein (beta APP), the microtubule associated
CC	proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule-
CC	associated protein 2 (MAP2), neurofilament-L, neurofilament-M,

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CC cell can be derived. The cDNA sequence encoding the peptide is a sense oriented genetic suppressor element (GSE) for reversing

CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present invention is a mutant

CC Bcl-2 protein of the invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 15.2%; Score 134; DB 22; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 5.8e-07;  
 Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;  
 QY 37 EYVHARLLRAGLSW-----SAPERASPARG----- 61  
 Db 17 KYIHKLAGSGYEMDADGAGAPGAPGIFSSQPGHPPHAPASDPVARTSPLOTPTA 76  
 QY 62 -----GRLAEVCTV 70  
 Db 77 APGAAGPALSPVPPVHVALRQAGDDFSRRYRGDFEAMSSQLHLTPPTARGREAVVEE 136  
 QY 71 LRLGITMGKVSLSYSAAGIADVCVRQAPAMVHALVDCIGFEVRKTLATWLRRGWT 130  
 Db 137 LFRDGVWNGRIIVAFEEGVCWCVESVAVNREMSPLVDNALMTEYLNHNLHTWIDNGWD 196  
 QY 131 DVLCV-VSTKPGFRSHWL-VATLCS 154  
 Db 197 AFVELYGPSMRPLDFEWSLSKTLIS 222  
 RESULT 13  
 AAG64038  
 ID AAG64038 standard; protein; 239 AA.  
 XX  
 AC AAG64038;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Human Bcl-2 protein mutant #3.  
 XX  
 KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200142459-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 07-DEC-2000; 2000WO-JP08667.  
 XX  
 PR 09-DEC-1999; 99JP-0350427.  
 XX  
 PA (HISM ) HISAMITSU PHARM CO LTD.  
 XX  
 PI Shibazaki F, Kuma H;  
 XX  
 DR WPI; 2001-381681/40.  
 XX  
 PT New apoptosis inhibitors, useful for treating apoptosis related  
 PT disorders -  
 XX  
 PS Claim 7; Page 33-34; 43pp; Japanese.  
 XX  
 CC The invention relates to an apoptosis inhibitor comprising the  
 CC amino acid sequence of Bcl-2 protein in which at least one serine  
 CC residue is substituted by alanine or aspartic acid. The protein has  
 CC increased apoptosis inhibitory activity compared with the wild type  
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment  
 CC of disorders caused by apoptosis. The present sequence is a mutant  
 CC Bcl-2 protein of the invention.  
 CC  
 SQ Sequence 239 AA;  
 Query Match 15.2%; Score 134; DB 22; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 5.8e-07;  
 Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;

QY 37 EYVHARLLRAGLSW-----SAPERASPARG----- 61  
 Db 17 KYIHKLAGSGYEMDADGAGAPGAPGIFSSQPGHPPHAPASDPVARTSPLOTPTA 76  
 QY 62 -----GRLAEVCTV 70  
 Db 77 APGAAGPALSPVPPVHVALRQAGDDFSRRYRGDFEAMSSQLHLTPPTARGREAVVEE 136  
 QY 71 LRLGITMGKVSLSYSAAGIADVCVRQAPAMVHALVDCIGFEVRKTLATWLRRGWT 130  
 Db 137 LFRDGVWNGRIIVAFEEGVCWCVESVAVNREMSPLVDNALMTEYLNHNLHTWIDNGWD 196  
 QY 131 DVLCV-VSTKPGFRSHWL-VATLCS 154  
 Db 197 AFVELYGPSMRPLDFEWSLSKTLIS 222  
 RESULT 14  
 AAP80987  
 ID AAP80987 standard; protein; 239 AA.  
 XX  
 AC AAP80987;  
 XX  
 DT 17-DEC-1990 (first entry)  
 XX  
 DE Sequence of bcl-2-alpha encoded by sequence of bcl-2 cDNA corresp. to  
 DE the 5.5 kb transcript.  
 XX  
 KW B-cell neoplasm; diagnosis; follicular lymphomas.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP252685-A.  
 XX  
 PD 13-JAN-1988.  
 XX  
 PF 02-JUL-1987; 87EP-0305863.  
 XX  
 PR 09-JUL-1986; 86US-0883687.  
 XX  
 PA (WIST-) WISTAR CORP.  
 XX  
 PI Tsujimoto Y, Croce CM;  
 XX  
 DR WPI; 1988-008633/02.  
 XX  
 DR N-PSDB; AAN81292.  
 XX  
 PT Detection of B-cell neoplasms -  
 PT by extn. of proteins or RNA from B-cells and quantitation using  
 PT specific antibody or DNA probe  
 XX  
 PS Claim 12; Fig 2A-2D; 23pp; English.  
 XX  
 CC A human bcl-2 gene substantially free of introns is claimed. Also  
 CC claimed is a substantially pure preparation of a protein having an  
 CC N-terminal end encoded by the first exon of the human bcl-2 gene wherein  
 CC said protein is bcl-2-alpha having about 239 (AAP80987) or 205 (AAP80988)  
 CC amino acid residues. B-cell neoplasms which are associated with t(14;18)  
 CC chromosome translocations cause an increase in expression of both the  
 CC c-myc and the protein products of the bcl-2 gene. This is used to detect  
 CC B-cell neoplasms including follicular lymphomas as well as other  
 CC lymphomas. Bacterial isolates available as ATCC 67147 and 67148 can be  
 CC used to express bcl-2 gene products alpha (AAN81292) and beta (AAN91293)  
 CC resp. in bacteria.  
 CC  
 SQ Sequence 239 AA;  
 Query Match 15.0%; Score 133; DB 9; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 7.5e-07;  
 Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;  
 QY 37 EYVHARLLRAGLSW-----SAPERASPARG----- 61

```

Db 17 KYIHYKLSQRYEMDAGVGAAPGAPAPGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76
Oy 62 -----GRLAEVCTV 70
Db 77 APGAAGPALSPVPPVHLALRQAGDDFSRRKRGDFAEMSSOLHTPTTARGRFATVVEE 136
Oy 71 LRLGITWGVSLYSAAGLAVDCVROAPAMVHALVDCIGEFVRKTLATWLRRRGGWT 130
Db 137 LFRDGVNMGRIYAFEFPGVCMVESVNRMSPLVDNIALMWTETYNRHLHTWIDQNGMD 196
Oy 131 DVLKCV-VSTKGFERSHML-VATLCS 154
Db 197 AFVELYGPSMRPLFDFSWLSLKTLLS 222

```

## RESULT 15

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ID AAR42312
AC AAR42312 standard; Protein; 239 AA.

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XX AAR42312;

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DT 03-MAY-1994 (first entry)

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DE Bcl-2 oncogene product.

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XX Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc.

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XX Homo sapiens.

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XX W09320200-A.

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XX 14-OCT-1993.

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XX 02-APR-1993; 93WO-GB00686.

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XX 02-APR-1992; 92GB-0007275.

```

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XX 02-APR-1992; 92GB-0007276.

```

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XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

```

```

XX Evan GI;

```

```

XX WPI; 1993-336908/42.

```

```

XX N-PSDB; AAQ49815.

```

```

PT Treating tumor cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing BCL-2

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```

XX Disclosure; Page 76-77; 109pp; English.

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```

CC A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.

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```

CC Myc-induced cell death can be de-inhibited in tumor cells by admin.
CC of bcl-2 antisense oligonucleotides.

```

```

XX Sequence 239 AA;

```

```

Query Match 15.0%; Score 133; DB 14; Length 239;
Best Local Similarity 19.4%; Pred. NO. 7.5e-07;
Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;

```

```

Oy 37 EYVHARLRLAGLSW-----SAPERASPAFC-----61
Db 17 KYIHYKLSQRYEMDAGVGAAPGAPAPGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76

```

```

Oy 62 -----GRLAEVCTV 70

```

```

Db 77 APGAAGPALSPVPPVHLALRQAGDDFSRRKRGDFAEMSSOLHTPTTARGRFATVVEE 136

```

```

Oy 71 LRLGITWGVSLYSAAGLAVDCVROAPAMVHALVDCIGEFVRKTLATWLRRRGGWT 130
Db 137 LFRDGVNMGRIYAFEFPGVCMVESVNRMSPLVDNIALMWTETYNRHLHTWIDQNGMD 196
Oy 131 DVLKCV-VSTKGFERSHML-VATLCS 154
Db 197 AFVELYGPSMRPLFDFSWLSLKTLLS 222

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